



Ser Pro Gly Ser Arg Cys His Lys Thr Met Arg Asn Cys Cys Thr Ser  
 50 55 60

Cys Ser Ser Tyr Lys Gly Lys Cys Arg Pro Arg Lys  
 65 70 75

<210> 3  
 <211> 30  
 <212> PRT  
 <213> Unknown

<220>  
 <223> unknown Conus species

<220>  
 <221> PEPTIDE  
 <222> (1)..(30)  
 <223> Xaa at residue 4 and 28 is Pro or Hyp; Xaa at residue 22 is Tyr,  
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T  
 Y

<400> 3  
 Cys Leu Ser Xaa Gly Ser Arg Cys His Lys Thr Met Arg Asn Cys Cys  
 1 5 10 15

Thr Ser Cys Ser Ser Xaa Lys Gly Lys Cys Arg Xaa Arg Lys  
 20 25 30

<210> 4  
 <211> 283  
 <212> DNA  
 <213> Unknown

<220>  
 <223> unknown Conus species

<400> 4  
 ggatccatga aactgacgtg cgtggtgatc gtcggcgtgc tgctcctgac ggtctgtcaa 60  
 ctcatcacag ctgatgactc cagaggtacg cagaagcatc atgcccctgag gtcgaccacc 120  
 aatttctcca cgtcgactcg tcgctgcaaa cctcccgaa gaaaatgtct gaatagaaaag 180  
 aatgaatgct gcagcaagtt ttgcaatgaa cacctacata tgtgtggata aatggctaaa 240  
 aactgaataa aagccgcatt gcaaaaaaaaaaaaaaaa aaa 283

<210> 5  
 <211> 74  
 <212> PRT  
 <213> Unknown

<220>  
 <223> unknown Conus species

<400> 5  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Val  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His His  
 20 25 30

Ala Leu Arg Ser Thr Thr Asn Phe Ser Thr Ser Thr Arg Arg Cys Lys  
 35 40 45

Pro Pro Gly Arg Lys Cys Leu Asn Arg Lys Asn Glu Cys Cys Ser Lys  
 50 55 60

Phe Cys Asn Glu His Leu His Met Cys Gly  
 65 70

<210> 6  
 <211> 27  
 <212> PRT  
 <213> Unknown

<220>  
 <223> unknown Conus species

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 14 and 22 is Glu or gamma-carboxy Glu; Xaa at resi  
 due 3 and 4 is Pro or Hy

<400> 6  
 Cys Lys Xaa Xaa Gly Arg Lys Cys Leu Asn Arg Lys Asn Xaa Cys Cys  
 1 5 10 15

Ser Lys Phe Cys Asn Xaa His Leu His Met Cys  
 20 25

<210> 7  
 <211> 275  
 <212> DNA  
 <213> Unknown

<220>  
 <223> unknown Conus species

<400> 7  
 gatatccatga aactgacgtg cgtggtgatc gtcggcgtgc tgctcctgac ggcctgtcaa 60  
 ctcgtcacag ctgatggctc cagaggtatg cagaagcatt atgccctgag gtcgaccacc 120  
 aatctctcca tatcgtctcg ctgcaaacct cccagaagaa aatgtotgaa gattaaggat 180  
 aatgtctgca acttttgc当地 tacacaccta aatatgtgtg gataaatggc taaaaactga 240  
 ataaaaagccg cattgcaaaa aaaaaaaaaa aaaaa 275

<210> 8  
 <211> 72  
 <212> PRT  
 <213> Unknown

<220>  
 <223> unknown Conus species

<400> 8  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Val Thr Ala Asp Gly Ser Arg Gly Met Gln Lys His Tyr  
 20 25 30

Ala Leu Arg Ser Thr Thr Asn Leu Ser Ile Ser Ser Arg Cys Lys Pro  
 35 40 45

Pro Arg Arg Lys Cys Leu Lys Ile Lys Asp Lys Cys Cys Asn Phe Cys  
50 55 60

Asn Thr His Leu Asn Met Cys Gly  
65 70

<210>	9
<211>	26
<212>	PRT
<213>	Unknown

<220>  
<223> unknown *Conus* species

<220>

<221> PEPTIDE

-<222>-(1)...(26)

<223> Xaa at residue 3 and 4 is Pro or Hyp

<400> 9

Cys Lys Xaa Xaa Arg Arg Lys Cys Leu Lys Ile Lys Asp Lys Cys Cys  
 1 5 10 15

Asn Phe Cys Asn Thr His Leu Asn Met Cys  
20 25

<210> 10  
<211> 377  
<212> DNA  
<213> Unknown

<220>  
<223> unknown *Conus* species

<400> 10

ggatccatga aactgacgtg tgggtgatc gtcgcctgtgc tgctcctgat ggcctgtcaa

60

ctcgtcacag ctgatggctc cagaggtatg cacaaggcatt atgccctgag gtcgaccacc 120

aaactctcca tqtgcactcq ctgcgcaggc ccaggaacaa tttgtcctaa tagggtatgc 180

taccaattttt qcaqtaaaaq aacacatcta tqtcatcgc qaactqgctq atcttcccccc 240

ttctgactc catcctttc tgcctgaaatc ctccataact gagaatggtc atgaaacct 300

caaacacccatc tcctctggaa ggcctcagaa gagctacatt gaaataaaaaa ccgcattaca 360

377

$\langle 310 \rangle = 11$

<211> /4  
<212> PPT

<213> Unknown

<223> unknown *Conus* species

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Met Ala  
1 5 10 15

Cys Gln Leu Val Thr Ala Asp Gly Ser Arg Gly Met His Lys His Tyr  
20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Ser Thr Arg Cys Ala Gly

35

40

45

Pro Gly Thr Ile Cys Pro Asn Arg Val Cys Cys Gly Tyr Cys Ser Lys  
 50 55 60

Arg Thr His Leu Cys His Ser Arg Thr Gly  
 65 70

<210> 12  
 <211> 28  
 <212> PRT  
 <213> Unknown

<220>  
 <223> unknown Conus species

<220>  
 <221> PEPTIDE  
 <222> (1)...(28)  
 <223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue 16 is Tyr, 1  
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 12  
 Cys Ala Gly Xaa Gly Thr Ile Cys Xaa Asn Arg Val Cys Cys Gly Xaa  
 1 5 10 15

Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr  
 20 25

<210> 13  
 <211> 323  
 <212> DNA  
 <213> Conus arenatus

<400> 13  
 ggatccatga aactgacgtg catggtgatc atcgccgtgc tggtcctgac ggcctgtcaa 60  
 ctcattacag gtgagcagaa ggaccatgct ctgaggtcaa ctgacaaaaaa ctccaagttg 120  
 actaggcagt gctcggtctaa cggtggtatct tgtactcgatc attttactg ctgcagcctc 180  
 tattgcaata aagattccag tgtatgtgtg gcaacctcat acccgtgagt ggccatgaac 240  
 ccctcaatac cctctccctct ggaggcttca gaggaactgc attgaaataa aaccgcattg 300  
 caataaaaaa aaaaaaaaaa aaa 323

<210> 14  
 <211> 73  
 <212> PRT  
 <213> Conus arenatus

<400> 14  
 Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr  
 20 25 30

Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Ser Ala Asn Gly Gly Ser  
 35 40 45

Cys Thr Arg His Phe His Cys Cys Ser Leu Tyr Cys Asn Lys Asp Ser  
 50 55 60

T00202000T0060

Ser Val Cys Val Ala Thr Ser Tyr Pro  
65 70

<210> 15  
<211> 33  
<212> PRT  
<213> Conus arenatus

<220>  
<221> PEPTIDE  
<222> (1)..(33)  
<223> Xaa at residue 1 is Gn or pyro-Glu; Xaa at residue 33 is Pro or H  
yp; Xaa at residue 19 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-  
iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 15

Xaa Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys  
1 5 10 15

Ser Leu Xaa Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Xaa  
20 25 30

Xaa

<210> 16  
<211> 326  
<212> DNA  
<213> Conus arenatus

<400> 16

acccaaaacca tcatcaaaat gaaactgacg tgcgtgttga ttatcgccgt gctgttcctg 60  
acggcctgtc aactcattac agctgagact tactccagag gtgagcagaa gcaccatgct

ctgaggtcaa ctgacagaaaa ctccaagttg accaggacat gcaacactcc cactgaatat 120  
tgtactttgc atcgacactg ctgcagcggc tactgccata aaacaatcca ggcatgttca

taataccggt gagtggtcat gaaccactca ataccctctc ctctggaggc ttcagaggaa 180  
ctgcattgaa ataaaagccg cattgc 240

300

<210> 17

<211> 74

<212> PRT

<213> Conus arenatus

<400> 17

Met Lys Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Lys His  
20 25 30

His Ala Leu Arg Ser Thr Asp Arg Asn Ser Lys Leu Thr Arg Thr Cys  
35 40 45

Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Arg His Cys Cys Ser Gly  
50 55 60

Tyr Cys His Lys Thr Ile Gln Ala Cys Ser  
65 70

<210> 18  
 <211> 28  
 <212> PRT  
 <213> Conus arenatus  
  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 5 is Pro or Hyp; Xaa at residue 8 and 19 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 18  
 Thr Cys Asn Thr Xaa Thr Xaa Xaa Cys Thr Leu His Arg His Cys Cys  
 1 5 10 15

Ser GIy Xaa Cys His Lys Thr Ile Gln Ala Cys Ser  
 20 25

<210> 19  
 <211> 332  
 <212> DNA  
 <213> Conus arenatus  
  
 <400> 19  
 accaaaaacca tcatcaaaat gaaactgacg tgcgtgtga tcatcgccgt gctgttcctg 60  
 acggcctgtc aactcattac agctgagact tactccagag gtgagcagat gcaccgtgct 120  
 ctgagggtcaa ctgacaaaaa ctccaagttg actaggcagt gcacgcctaa cggtgatct 180  
 ttttctcgtc attttcaactg ctgcagcctc tattgcaata aaagtactgg cgtatgtatt 240  
 gcaacctcat acccgtgagt ggtcatgaac cactcaatac cctctcctct ggaggcttca 300  
 gaggaactgc attgaaataa aagccgcatt gc 332

<210> 20  
 <211> 79  
 <212> PRT  
 <213> Conus arenatus

<400> 20  
 Met Lys Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Met His  
 20 25 30

Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys  
 35 40 45

Thr Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys Ser Leu  
 50 55 60

Tyr Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Tyr Pro  
 65 70 75

<210> 21  
 <211> 33  
 <212> PRT  
 <213> Conus arenatus  
  
 <220>  
 <221> PEPTIDE

F0E22000T650

<222> (1)..(33)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 and 33 is P  
 ro or Hyp; Xaa at residue 19 and 32 is Tyr, 125I-Tyr, mono-iodo-T  
 yr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 21  
 Xaa Cys Thr Xaa Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys  
 1 5 10 15  
 Ser Leu Xaa Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Xaa  
 20 25 30

Xaa

---

<210> 22  
 <211> 332  
 <212> DNA  
 <213> Conus arenatus

<400> 22  
 ggatccatga aactgacgtg catggtgatt atcgccgtgc tggtcctgac ggcctgtcaa 60  
 ctcattacag ctgagactta ctccagaggt gagcagaagc accatgctct gaggtcaact 120  
 gacaaaaact ccaagttgac caggacatgc aacactccca ccgaatattg tactttgcat 180  
 caacactgct gcagcggcta ctgccataaa acaatccagg catgttcata ataccggta 240  
 gtggtcatga accactcaat accctctcct ctggaggctt cagaggaact gcattgaaat 300  
 aaaaccgcat tacaaaaaaaaaaaaaa aa 332

<210> 23  
 <211> 74  
 <212> PRT  
 <213> Conus arenatus

<400> 23  
 Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Lys His  
 20 25 30

His Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Thr Cys  
 35 40 45

Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Gln His Cys Cys Ser Gly  
 50 55 60

Tyr Cys His Lys Thr Ile Gln Ala Cys Ser  
 65 70

<210> 24  
 <211> 28  
 <212> PRT  
 <213> Conus arenatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 5 is  
 Pro or Hyp; Xaa at residue 8 and 19 is Tyr, 125I-Tyr, mono-iodo-  
 Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 24  
 Thr Cys Asn Thr Xaa Thr Xaa Xaa Cys Thr Leu His Gln His Cys Cys  
 1 5 10 15

Ser Gly Xaa Cys His Lys Thr Ile Gln Ala Cys Ser  
 20 25

<210> 25

<211> 394

<212> DNA

<213> Conus arenatus

<400> 25

ggatccatga aactgacgtg tatggtgatc atcgccgtac tgttcctgac ggcctgtcaa 60

ctcattacag ctgagactta ctccagaggt aagcagatgc accgcgtct gaggtcaact 120

gacaaaaact cccagttgac cagggaatgc acacctcccg gtggagcttgg 180

acacactgct gcgggttttgc cgatactgca aacaacagat gtctgtaaag ctgggtctggc 240

gtctgatatt ccccttctgt gctctatcct ctttggcctg agtcatccgt acctgtgagt 300

ggtcatgaac tactcaatac cctctccctc ggaggcgttca gaggaactac aatgaaataa 360

aacccgcatt gcagagaaaa aaaaaaaaaa aaaa 394

<210> 26

<211> 73

<212> PRT

<213> Conus arenatus

<400> 26

Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Met His  
 20 25 30

Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Gln Leu Thr Arg Glu Cys  
 35 40 45

Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys Gly Phe  
 50 55 60

Cys Asp Thr Ala Asn Asn Arg Cys Leu  
 65 70

<210> 27

<211> 27

<212> PRT

<213> Conus arenatus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa at residue 4, 5  
 and 12 is Pro or Hy

<400> 27

Xaa Cys Thr Xaa Xaa Gly Gly Ala Cys Gly Leu Xaa Thr His Cys Cys  
 1 5 10 15

Gly Phe Cys Asp Thr Ala Asn Asn Arg Cys Leu

20

25

<210> 28  
 <211> 345  
 <212> DNA  
 <213> Conus arenatus

<220>  
 <221> misc\_feature  
 <222> (1)..(345)  
 <223> n may be any nucleotide

<400> 28  
 ggatccatga aactgacgtg cgtggtgatt atcgccgtgc tgttcctgac ggccgtcaa 60

~~ctcattacag ctqagactta ctccagaggt gaggcagaatc accatgttct gaggtcaact~~ 120  
 gacaaaaact ccaagttgac caggacatgc aacactccca ctgaatattt tactttgcat 180  
 caacactgct gcagcggcca ctgccataaa acaatccagg catgtgcata ataccgggtgg 240  
 gtggtcatga accactcaat accctctcct ctggaggctt cagaggaact gcattgaaat 300  
 aaaaccgcat tgcaatgaan aaaaaaaaaa aaaaaaaaaa aaaaa 345

<210> 29  
 <211> 74  
 <212> PRT  
 <213> Conus arenatus

<400> 29  
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala 1  
 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Asn His  
 20 25 30

His Val Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Thr Cys  
 35 40 45

Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Gln His Cys Cys Ser Gly  
 50 55 60

His Cys His Lys Thr Ile Gln Ala Cys Ala  
 65 70

<210> 30  
 <211> 28  
 <212> PRT  
 <213> Conus arenatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 5 is Pro or Hyp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 30  
 Thr Cys Asn Thr Xaa Thr Xaa Xaa Cys Thr Leu His Gln His Cys Cys  
 1 5 10 15

Ser Gly His Cys His Lys Thr Ile Gln Ala Cys Ala  
 20 25

<210> 31  
 <211> 322  
 <212> DNA  
 <213> Conus arenatus

<400> 31  
 ggatccatga aactgacgtg tgtggtgatc atcgccgtgc tgccctgac ggcctgtcaa 60  
 ctcactacag gtgagcagaa ggaccatgct ctgaggtcaa ctgacaaaaa ctccaagttg 120  
 actaggcagt gctcgccat cggatgatat tgtactcttc atattcactg ctgcagcaac 180  
 cattgcatta aacatatcgg ccgatgtgtg gcaacctgat acccgtgcgt ggtcatgaac 240  
 ccctcaatac cctctccctc ggaggcttca gaggaactgc attgaaataa aaccgcattg 300  
 caataaaaaa aaaaaaaaaa aa

322

<210> 32  
 <211> 70  
 <212> PRT  
 <213> Conus arenatus

<400> 32  
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Thr Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr  
 20 25 30  
 Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Ser Pro Ile Gly Gly Tyr  
 35 40 45  
 Cys Thr Leu His Ile His Cys Cys Ser Asn His Cys Ile Lys Pro Ile  
 50 55 60  
 Gly Arg Cys Val Ala Thr  
 65 70

<210> 33  
 <211> 30  
 <212> PRT  
 <213> Conus arenatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(30)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 and 23 is P  
 ro or Hyp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-i  
 odo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 33  
 Xaa Cys Ser Xaa Ile Gly Gly Xaa Cys Thr Leu His Ile His Cys Cys  
 1 5 10 15  
 Ser Asn His Cys Ile Lys Xaa Ile Gly Arg Cys Val Ala Thr  
 20 25 30

<210> 34  
 <211> 318  
 <212> DNA  
 <213> Conus arenatus

<400> 34  
 ggatccatga aactgacgtg cgtggtgatc atcgccgtgc tgccctgac ggcctgtcaa 60

ctcactacag gtgagcagaa ggaccatgct ctgaggtcaa ctgacaaaaaa ctccaagttg	120
actaggcagt gcttcctaa cggtgatata tgtactcttc atattcactg ctgcagcgac	180
cattgcatta aacctatcga ccgatgtgtg gcaacctgat accccggcgt ggtcatgaac	240
ccctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcatta	300
aaaaaaaaaa aaaaaaaaaa	318
<210> 35	
<211> 70	
<212> PRT	
<213> <i>Conus arenatus</i>	

<400> 35  
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Cys Gln Leu Thr Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr  
20 25 30

Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Leu Pro Asn Gly Gly Tyr  
35 40 45

Cys Thr Leu His Ile His Cys Cys Ser Asp His Cys Ile Lys Pro Ile  
50 55 60

Asp Arg Cys Val Ala Thr  
65 70

<210> 36

<211> 30

<212> PRT

<213> Conus arenatus

<220>

<221> PEPTIDE

<222> (1)..(30)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 and 23 is P  
ro or Hyp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-i  
odo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 36

Xaa Cys Leu Xaa Asn Gly Gly Xaa Cys Thr Leu His Ile His Cys Cys  
1 5 10 15

Ser Asp His Cys Ile Lys Xaa Ile Asp Arg Cys Val Ala Thr  
20 25 30

<210> 37

<211> 374

<212> DNA

<213> Conus aurisiacus

<400> 37

atgaaaactga cgtgtgtggg qatcgtccacc gtatctactcc tgggggggtt ..

aaatgtttttt aatcccaaggagg tacgcagaag catcggttcccc tgagctcggc cacccaaactc

tccatgtcga ctcgctgcaa gggtaaagga aaaccatgca gtaggattt cttatccatc 300

tgcacccgatt ctttgatgc aggtttatgtt -

tgtgctctat ccttttctgc ctgagtcctc cttacctgag agtggtcatg aaccactcat 300  
 cacctgctcc tctggaggcc ccagaggagc tacattgaaa taaaagtgcg attgcaaaaa 360  
 aaaaaaaaaa aaaa  
 374

<210> 38  
 <211> 71  
 <212> PRT  
 <213> Conus aurisiacus

<400> 38  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

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Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ser Leu Ser Ser Ala Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly  
 35 40 45

Lys Gly Lys Pro Cys Ser Arg Ile Ser Tyr Asn Cys Cys Thr Gly Ser  
 50 55 60

Cys Arg Ser Gly Lys Cys Gly  
 65 70

<210> 39  
 <211> 25  
 <212> PRT  
 <213> Conus aurisiacus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Ty  
 r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 39  
 Cys Lys Gly Lys Gly Lys Xaa Cys Ser Arg Ile Ser Xaa Asn Cys Cys  
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
 20 25

<210> 40  
 <211> 380  
 <212> DNA  
 <213> Conus aurisiacus

<400> 40  
 atgaaaactga cgtgtgtggc gatcgctgcc gtgctgctcc tgacggcctg tcaactcatc 60  
 acagctgatg actccagagg tacgcagaag catcgatccc tgaggtcgaa gaccaaactc  
 tccatgtcga ctggctgcat ggaagccgga tcttattgcg gctctactac gagaatctgc 120  
 tgcggttttt gcgcttattt cggcaaaaaa tgtattgact atcccagcaa ctgatctcc  
 ccctactgtg ctctatcctt ttctgcctga gtcctcctta cctgagagtg gtcatgaacc 180  
 actcatcacc tgctcctctg gaggccccag aggagctaca ttgaaataaa atcgattgc  
 taaaaaaaaa aaaaaaaaaa  
 360  
 380

<210> 41  
 <211> 77  
 <212> PRT  
 <213> Conus aurisiacus

<400> 41  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ser Leu Arg Ser Lys Thr Lys Leu Ser Met Ser Thr Gly Cys Met Glu  
 35 40 45

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Ala Gly Ser Tyr Cys Gly Ser Thr Thr Arg Ile Cys Cys Gly Phe Cys  
 50 55 60

Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr Pro Ser Asn  
 65 70 75

<210> 42  
 <211> 32  
 <212> PRT  
 <213> Conus aurisiacus

<220>  
 <221> PEPTIDE  
 <222> (1)..(32)  
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 30 is Pro or Hyp; Xaa at residue 7, 21 and 29 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 42  
 Cys Met Xaa Ala Gly Ser Xaa Cys Gly Ser Thr Thr Arg Ile Cys Cys  
 1 5 10 15

Gly Phe Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa Xaa Ser Asn  
 20 25 30

<210> 43  
 <211> 373  
 <212> DNA  
 <213> Conus aurisiacus

<400> 43  
 accaaaacca tcatcaaaat gaaaactgacg tgtgtggta tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac agctgatgac tccagaggta cgccagaagca tcgttccctg 120  
 agctcggcca ccaaactctc catgtcgact cgctgcaagg ctaaaggaaa accatgcagt 180  
 aggattgcgt ataactgctg caccggttct tgcagatcag gtaaatgtgg ctgatccagt 240  
 gcctgatctt cccccttctg tgctctatcc ttttctgcct gagtcctcct tacctgagag 300  
 tggtcatgaa ccactcatca cctgctcctc tggaggcccc agaggagcta cattgaaata 360  
 aaagccgcat tgc 373

<210> 44  
 <211> 71  
 <212> PRT  
 <213> Conus aurisiacus

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<400> 44
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1           5           .           10          15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20          25          .           30
Ser Leu Ser Ser Ala Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ala
35          40          .           45
Lys Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser
50          55          .           60
Cys Arg Ser Gly Lys Cys Gly
65          70

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<210> 45
<211> 25
<212> PRT
<213> Conus aurisiacus

<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Ty
      r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
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<400> 45  
 Cys Lys Ala Lys Gly Lys Xaa Cys Ser Arg Ile Ala Xaa Asn Cys Cys  
 1 5 10 15  
 Thr Gly Ser Cys Arg Ser Gly Lys Cys  
 20 25

<210> 46  
<211> 379  
<212> DNA  
<213> *Conus aurisiacus*

<400> 46 accaaaacca tcatcaaaat gaaactgacg tgtgtggta tcgtcgccgt gctgctcctg 60  
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aggtcgaaga caaaaactctc catgttaact ttgcgcgtcg catcttacgg aaaaccttgt 180  
ggtattgaca acgactgctg caatgcattgc gatccaggaa gaaatataatg tacgttagctg 240  
atccagcgcc tgatcttccc cttctgtgc tctatccttt tctgcccggag tcctccttac 300  
ctgagagtgg tcatgaacca ctcatcacct gctccctggaa ggcctcagag gagctacaat 360  
gaaataaaag ccgcattgc 379

<210> 47  
<211> 72  
<212> PRT  
<213> *Conus aurisiacus*

<400> 47  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr  
1 5 10 15  
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg  
20 25 30

Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala  
 35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Ala Cys  
 50 55 60

Asp Pro Gly Arg Asn Ile Cys Thr  
 65 70

<210> 48  
 <211> 26  
 <212> PRT  
 <213> Conus aurisiacus

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1  
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 48  
 Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn  
 1 5 10 15

Ala Cys Asp Xaa Gly Arg Asn Ile Cys Thr  
 20 25

<210> 49  
 <211> 382  
 <212> DNA  
 <213> Conus bullatus

<400> 49  
 accaaaaacca tcatcaaaat gaaactgacg tgtgtggcga tcgtcgccgt gctgctcctg 60  
 acggcctgtc agctcattac agctgaagac tccagaggta cgcatgagca tcttgccctg 120  
 aagtcgacct ccaaagtctc caagtcgact agctgcattg aagccggatc ttattgcgga 180  
 cctgctacta cgaaaaatctg ctgcgattt tgcaagtccat tcagcgatag atgtatgaac 240  
 aatccccaca attgatctc ccccttgtgt gctccatcct tttctgcctg agtcctcctt 300  
 acctgagagt ggtcatgaac cactcatcac ctactcctct ggaggcattca gaggagctac 360  
 attgaaataa aagccgcatt gc 382

<210> 50  
 <211> 78  
 <212> PRT  
 <213> Conus bullatus

<400> 50  
 Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu  
 20 25 30

Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Glu  
 35 40 45

Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr Lys Ile Cys Cys Asp Phe

50

55

60

Cys Ser Pro Phe Ser Asp Arg Cys Met Asn Asn Pro Asn Asn  
 65 70 75

<210> 51  
 <211> 36  
 <212> PRT  
 <213> Conus bullatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(36)  
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13,  
 25 and 34 is Pro or Hyp; Xaa at residue 10 is Tyr, 125I-Tyr, mono  
-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 51  
 Ser Thr Ser Cys Met Xaa Ala Gly Ser Xaa Cys Gly Xaa Ala Thr Thr  
 1 5 10 15

Lys Ile Cys Cys Asp Phe Cys Ser Xaa Phe Ser Asp Arg Cys Met Asn  
 20 25 30

Asn Xaa Asn Asn  
 35

<210> 52  
 <211> 400  
 <212> DNA  
 <213> Conus bullatus

<400> 52  
 accaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60  
 acggcctgtc agtcattac agctgaagac tccagaggta cgcatgtca tcgtgccctg 120  
 aggaaggcca ccaaacaccc tgtgtcgact cgctgcatta ctccaggaac acgatgttaag 180  
 gttccgagcc aatgctgcag aggtccttgc aagaacggc gttgtactcc atccccttct 240  
 gaatggtaaa tgtggttgat ccagcgctg atttcccccc ttctgtgtgc tccatcctt 300  
 tctgcctgag tcctccttac ctgagagtgg tcatgaacca ctcacacct actcccctgg 360  
 aggcttcaga ggagctacat taaaataaaa gcccattgc 400

<210> 53  
 <211> 76  
 <212> PRT  
 <213> Conus bullatus

<400> 53  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg  
 20 25 30

Ala Leu Arg Lys Ala Thr Lys His Pro Val Ser Thr Arg Cys Ile Thr  
 35 40 45

Pro Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg Gly Pro Cys  
 50 55 60

Lys Asn Gly Arg Cys Thr Pro Ser Pro Ser Glu Trp  
 65 70 75

<210> 54  
 <211> 31  
 <212> PRT  
 <213> Conus bullatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(31)  
 <223> Xaa at residue 30 is Glu or gamma-carboxy Glu; Xaa at residue 4,  
 11, 18, 26 and 28 is Pro or Hyp; Xaa at residue 31 is Trp or Bromo  
 Tr

<400> 54

Cys Ile Thr Xaa Gly Thr Ala Cys Lys Val Xaa Ser Gln Cys Cys Arg  
 1 5 10 15

Gly Xaa Cys Lys Asn Gly Arg Cys Thr Xaa Ser Xaa Ser Xaa Xaa  
 20 25 30

<210> 55  
 <211> 379  
 <212> DNA  
 <213> Conus bullatus

<400> 55

acccaaaacca tcatcaaaat gaaactgacg tgggtggcga tcgtcgccgt gctgctcctg 60  
 acggcctgtc agctcattac agctgaggac tccagagata cgcagaagca tcgtgcccctg 120  
 aggtcggaca ccaaactctc catgttgact ttgcgctgctg caacttacgg aaaaaccttgt 180  
 ggtattcaaa acgactgctg caatacatgc gatccagcca gaaggacatg tacgttagctg 240  
 atccggcgtc ttgatccctcc gcttctgtgc tccatcttt ctgcctgagt cctccttacc 300  
 tgagagtggc catgaaccac tcatcaccta ctccctgtgg aagtttagag gagtacatt 360  
 gaaaataaaag ccgcattgc 379

<210> 56  
 <211> 72  
 <212> PRT  
 <213> Conus bullatus

<400> 56

Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Asp Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala  
 35 40 45

Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn Asp Cys Cys Asn Thr Cys  
 50 55 60

Asp Pro Ala Arg Arg Thr Cys Thr  
 65 70

<210> 57  
 <211> 26

<212> PRT  
 <213> Conus bullatus  
  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1  
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 57  
 Cys Ala Thr Xaa Gly Lys Xaa Cys Gly Ile Gln Asn Asp Cys Cys Asn  
 1 5 10 15  
 Thr Cys Asp Xaa Ala Arg Arg Thr Cys Thr  
 20 25

<210> 58  
 <211> 373  
 <212> DNA  
 <213> Conus bullatus  
  
 <400> 58  
 accaaaacca tcatcaaaat gaaactgacg tgggtggcga tcgtcgccgt gctgctcctg 60  
 acggcctgtc agctcattac agctgaagac tccagaggtt cgcagttgca tcgtgcctcg  
 aggaagacca ccaaactctc cttgtcgact cgctgcaagg gtccaggagc atcatgtata 120  
 aggattgcgt ataaactgctg caagtattct tgcagaaatg gttaatgtgg ctgatccagc  
 gcctgatctt ccccttgtg tgctccatcc ttttctgcct gagtcctcct tacctgagag 180  
 tggtcatgaa ccactcatca cctactcctc tggaggcttc agaggagcta cattgaaata 240  
 aaagccgcat tgc 300  
 360  
 373

<210> 59  
 <211> 71  
 <212> PRT  
 <213> Conus bullatus

<400> 59  
 Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg  
 20 25 30  
 Ala Leu Arg Lys Thr Thr Lys Leu Ser Leu Ser Thr Arg Cys Lys Gly  
 35 40 45

Pro Gly Ala Ser Cys Ile Arg Ile Ala Tyr Asn Cys Cys Lys Tyr Ser  
 50 55 60

Cys Arg Asn Gly Lys Cys Gly  
 65 70

<210> 60  
 <211> 25  
 <212> PRT  
 <213> Conus bullatus

<220>  
 <221> PEPTIDE

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<222> (1)..(25)  
 <223> Xaa at residue 4 is Pro or Hyp; Xaa at residue 13 and 18 is Tyr,  
       125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T  
       y  
  
 <400> 60  
 Cys Lys Gly Xaa Gly Ala Ser Cys Ile Arg Ile Ala Xaa Asn Cys Cys  
   1              5                 10                         15  
  
 Lys Xaa Ser Cys Arg Asn Gly Lys Cys  
   20                 25  
  
 <210> 61  
 <211> 382  
 <212> DNA  
 <213> Conus bullatus

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<400> 61  
 atcaaaacca tcatcaaaat gaaactgacg tgggtggta tcgtcgccgt gctgctcctg   60  
 acggcctgtc agtcattac agctgaagac tccagaggtt cgcatttttttgcctg   120  
 aagtcgacct ccaaagtctc caagtcgact agctgcatttttgccttgcggatc   180  
 cctgctacta cgaatatctg ctgcgattttt tgcaaggatccat tcagcgatag atgtatgaaa   240  
 aagcccaaca attgatcttc cccttctgt gctctatcct tttctgcctg agtcctcctt   300  
 acctgagagt ggtcatgaac cactcatcac ctactcctct ggaggcattca gaggagctac   360  
 attgaaataa aagccgcatt gc   382

<210> 62  
 <211> 78  
 <212> PRT  
 <213> Conus bullatus

<400> 62  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
   1              5                 10                         15  
  
 Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu  
   20                 25   30  
  
 Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Ala  
   35                 40   45  
  
 Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr Asn Ile Cys Cys Asp Phe  
   50                 55   60  
  
 Cys Ser Pro Phe Ser Asp Arg Cys Met Lys Lys Pro Asn Asn  
   65                 70   75

<210> 63  
 <211> 36  
 <212> PRT  
 <213> Conus bullatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(36)  
 <223> Xaa at residue 13, 25 and 34 is Pro or Hyp; Xaa at residue 10 is  
       Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos  
       pho-Ty

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<400> 63
Ser Thr Ser Cys Met Ala Ala Gly Ser Xaa Cys Gly Xaa Ala Thr Thr
1           5                   10                   15

Asn Ile Cys Cys Asp Phe Cys Ser Xaa Phe Ser Asp Arg Cys Met Lys
20          25                   30

Lys Xaa Asn Asn
35

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<210> 64  
<211> 373  
<212> DNA  
<213> *Conus bullatus*

<4.00> 64  
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acggccctgtc agtcattat agctgaggac tccagaggtt cgcagttgca tcgtgccctg 120  
aggaaggcca ccaaactctc cgtgtcgact cgctgcaaga gtaaaggatc atcatgtcat 180  
aggacttcgt atgactgctg cacgggttct tgcagaaaatg gtatgtgtgg ctgatccagc 240  
gcctgatctt cccccttctg tgctccatcc ttttctgcct gagtcctcct tacctgagag 300  
tggtcatgaa ccactcatca cctactcctc tggaggcttc agaggagcta cattgaaata 360  
aaagccgcat tgc 373

<210> 65  
<211> 71  
<212> PRT  
<213> *Conus bullatus*

<400> 65  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 . 10 15

Cys Gln Leu Ile Ile Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg  
20 25 30

Ala Leu Arg Lys Ala Thr Lys Leu Ser Val Ser Thr Arg Cys Lys Ser  
35 40 45

Cys Arg Asn Gly Arg Cys Gly  
65 70

<210> 66  
<211> 25  
<212> PRT  
<213> *Conus bullatus*

<220>  
<221> PEPTIDE  
<222> (1)..(25)  
<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 66  
Cys Lys Ser Lys Gly Ser Ser Cys His Arg Thr Ser Xaa Asp Cys Cys  
1 5 10 15

Thr Gly Ser Cys Arg Asn Gly Arg Cys  
20 25

<210> 67  
<211> 321  
<212> DNA  
<213> Conus characteristicus

<400> 67  
ggatccatga aactgacgtg cgtggtgatc atcgccgtgc tgttcctgac ggccgtgtcaa 60  
ctcattacag gtgagcagaa ggaccatgct ctgaggtcaa ctgacaaaaaa ctccaaaggtt 120  
actaggcagt gctcggctaa cggtggatct tgtactcgac attttcaactg ctgcagcctc 180  
tattgcaata aagattccag tgtatgtgtg gcaacctcat acccgtgagt ggccatgaac 240  
ccctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcatta 300  
caaaaaaaaaa aaaaaaaaaa a 321

<210> 68  
<211> 73  
<212> PRT  
<213> Conus characteristicus

<400> 68  
Met Lys Leu Thr Cys Val Val Ile Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr  
20 25 30

Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Ser Ala Asn Gly Gly Ser  
35 40 45

Cys Thr Arg His Phe His Cys Cys Ser Leu Tyr Cys Asn Lys Asp Ser  
50 55 60

Ser Val Cys Val Ala Thr Ser Tyr Pro  
65 70

<210> 69  
<211> 33  
<212> PRT  
<213> Conus characteristicus

<220>  
<221> PEPTIDE  
<222> (1)..(33)  
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 33 is Pro or  
Hyp; Xaa at residue 19 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-  
-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 69  
Xaa Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys  
1 5 10 15

Ser Leu Xaa Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Xaa  
20 25 30

Xaa

TOP SECRET

<210> 70  
 <211> 26  
 <212> PRT  
 <213> Conus catus

<400> 70  
 Cys Lys Ser Thr Gly Ala Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys  
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Arg Cys Gly  
 20 25

<210> 71  
 <211> 25  
 <212> PRT  
 <213> Conus catus

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<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 71  
 Cys Lys Ser Thr Gly Ala Ser Cys Arg Arg Thr Ser Xaa Asp Cys Cys  
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Arg Cys  
 20 25

<210> 72  
 <211> 229  
 <212> DNA  
 <213> Conus catus

<400> 72  
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 ctatcctttt ctgcctgatt cctccttacc tgagagcggt catgaaccac tcatacacctg 180  
 ctccctctgga ggcctcagag gagctacatt gaaataaaag ccgcattgc 229

<210> 73  
 <211> 29  
 <212> PRT  
 <213> Conus catus

<400> 73  
 Ser Thr Arg Cys Gln Gly Arg Gly Ala Ser Cys Arg Lys Thr Met Tyr  
 1 5 10 15

Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Ser Cys Gly  
 20 25

<210> 74  
 <211> 25  
 <212> PRT  
 <213> Conus catus

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<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O

-sulpho-Tyr or O-phospho-Ty

<400> 74  
 Cys Gln Gly Arg Gly Ala Ser Cys Arg Lys Thr Met Xaa Asn Cys Cys  
 1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Ser Cys  
 20 25

<210> 75  
 <211> 235  
 <212> DNA  
 <213> Conus catus

<400> 75  
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 tgtgctccat cctttctgc ctgagtcctc cttatctgag agtggtcatg aaccactcac 180  
 cacctactct tctggaggct tcagaggagc tacagtgaaa taaaagccgc attgc 235

<210> 76  
 <211> 31  
 <212> PRT  
 <213> Conus catus

<400> 76  
 Ser Thr Arg Cys Leu Pro Ala Gly Glu Ser Cys Leu Phe Ser Arg Ile  
 1 5 10 15  
 Arg Cys Cys Gly Thr Cys Ser Ser Val Leu Lys Ser Cys Val Ser  
 20 25 30

<210> 77  
 <211> 28  
 <212> PRT  
 <213> Conus catus

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 3 is  
 Pro or Hy

<400> 77  
 Cys Leu Xaa Ala Gly Xaa Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys  
 1 5 10 15

Gly Thr Cys Ser Ser Val Leu Lys Ser Cys Val Ser  
 20 25

<210> 78  
 <211> 227  
 <212> DNA  
 <213> Conus catus

<400> 78  
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 ctatcctttt ctgcctgagt ctccttact gagagtatc atgaaccact catcacctac 180

tcctctggag gcctcagaga gctacattga aataaaagcc gcattgc 227  
 <210> 79  
 <211> 29  
 <212> PRT  
 <213> Conus catus

<400> 79  
 Ser Thr Arg Cys Gln Gly Arg Gly Gly Pro Cys Thr Lys Ala Val Phe  
 1. 5 10 15

Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Arg Cys Gly  
 20 25

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<210> 80  
 <211> 25  
 <212> PRT  
 <213> Conus catus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 7 is Pro or Hyp

<400> 80  
 Cys Gln Gly Arg Gly Gly Xaa Cys Thr Lys Ala Val Phe Asn Cys Cys  
 1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Arg Cys  
 20 25

<210> 81  
 <211> 236  
 <212> DNA  
 <213> Conus catus

<400> 81  
 ttaactttgc gctgcgcaac ttacggaaaa ccttgtggta ttcaaaacga ctgctgcaat 60  
 acatgcgatc cagccagaaa gacatgtacg tagctgatcc ggcgtctgat ctccccccctt 120  
 ctgtgctcta tcctttctg cctgagtcct ccttacctga gagtggtcat gaaccactca 180  
 tcacctgctc ctctggaggc ctcggggagc ctacattgaa ataaaagccg cattgc 236

<210> 82  
 <211> 30  
 <212> PRT  
 <213> Conus catus

<400> 82  
 Leu Thr Leu Arg Cys Ala Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn  
 1 5 10 15

Asp Cys Cys Asn Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr  
 20 25 30

<210> 83  
 <211> 26  
 <212> PRT  
 <213> Conus catus

<220>  
 <221> PEPTIDE

F00E2400:2000000000000000

<222> (1)..(26)  
 <223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1  
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 83  
 Cys Ala Thr Xaa Gly Lys Xaa Cys Gly Ile Gln Asn Asp Cys Cys Asn  
 1 5 10 15  
 Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr  
 20 25

<210> 84

<211> 229

<212> DNA

<213> Conus catus

<400> 84  
 tcgactcgct gccggggtag aggaggacca tgtactaagg ctatgtttaa ctgctgcagc 60  
 ggttcttgca acagaggtag atgtggctga tccagcgct gatcttcccc cttctgtgct 120  
 ctatcctttt ctgcctgagt cctccttaac tgagagtagt catgaaccac tcatcaccta 180  
 ctcctctgga ggcctcagag aagcatcatt gaaataaaag ccgcattgc 229

<210> 85

<211> 29

<212> PRT

<213> Conus catus

<400> 85  
 Ser Thr Arg Cys Arg Gly Arg Gly Gly Pro Cys Thr Lys Ala Met Phe  
 1 5 10 15

Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Arg Cys Gly  
 20 25

<210> 86

<211> 25

<212> PRT

<213> Conus catus

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 7 is Pro or Hyp

<400> 86

Cys Arg Gly Arg Gly Gly Xaa Cys Thr Lys Ala Met Phe Asn Cys Cys  
 1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Arg Cys  
 20 25

<210> 87

<211> 374

<212> DNA

<213> Conus circumcisus

<400> 87

acccaaaacca tcatcaaaat gaaactgacg tgtgtggta tcgtcgccgt gctgctcctg 60  
 acgacctgtc aactcatcac agctgatgac tccagaggtt cgcaggagca tcgtgcccctg 120

TDBE2002-07-06

aggtcggaca ccaaactccc catgtcgact cgctgcaagg gtaaaggagc atcatgtcgt 180  
 aagactatgt ataactgctg cagcggttct tgcatcgaaacg gtagatgtgg ctgatccagc 240  
 gcctgatctt ccccttctg ctgctctatc ctttctgcc tgagtccctcc ttacctgaga 300  
 gctggtcatg aaccactcat cacctgctcc tctggaggcc cagaggagct acattgaaat 360  
 aaaagccgca ttgc  
 374

<210> 88  
 <211> 71  
 <212> PRT  
 <213> Conus circumcisus

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<400>—88  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg  
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Pro Met Ser Thr Arg Cys Lys Gly  
 35 40 45

Lys Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys Ser Gly Ser  
 50 55 60

Cys Ser Asn Gly Arg Cys Gly  
 65 70

<210> 89  
 <211> 25  
 <212> PRT  
 <213> Conus circumcisus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 89  
 Cys Lys Gly Lys Gly Ala Ser Cys Arg Lys Thr Met Xaa Asn Cys Cys  
 1 5 10 15

Ser Gly Ser Cys Ser Asn Gly Arg Cys  
 20 25

<210> 90  
 <211> 379  
 <212> DNA  
 <213> Conus circumcisus

<400> 90  
 accaaaaacca tcatcaaaat gaaactgacg tgtgtggta tcgtcgccgt gctgctcctg 60  
 acgacctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120  
 aggtcggcca ccaaagtctc caagtcgact agctgcattgg aagccggatc ttattgccgc 180  
 tctactacga gaacctgctg cggatttgc tcttatttca gcaaaaaatg tattgacttt 240  
 cccagcaact gatctcccc ctactgtgct ctatccttt ctgcctgagt cctccttacc 300

tgagagtgg catgaaccac tcatcacccct actcctctgg aggcccagag gagctacatt 360  
 gaaataaaag ccgcattgc 379  
 <210> 91  
 <211> 77  
 <212> PRT  
 <213> Conus circumcisus

<400> 91  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr  
 1 5 10 15

Cys	Gln	Leu	Ile	Thr	Ala	Asp	Asp	Ser	Arg	Gly	Thr	Gln	Lys	His	Arg
20								25				30			

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Ala Leu Arg Ser Ala Thr Lys Val Ser Lys Ser Thr Ser Cys Met Glu  
 35 40 45

Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg Thr Cys Cys Gly Tyr Cys  
 50 55 60

Ser Tyr Phe Ser Lys Lys Cys Ile Asp Phe Pro Ser Asn  
 65 70 75

<210> 92  
 <211> 35  
 <212> PRT  
 <213> Conus circumcisus

<220>  
 <221> PEPTIDE  
 <222> (1)..(35)  
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21 and 24 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 92  
 Ser Thr Ser Cys Met Xaa Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg  
 1 5 10 15

Thr	Cys	Cys	Gly	Xaa	Cys	Ser	Xaa	Phe	Ser	Lys	Lys	Cys	Ile	Asp	Phe
	20					25						30			

Xaa Ser Asn  
 35

<210> 93  
 <211> 379  
 <212> DNA  
 <213> Conus circumcisus

<400> 93  
 accaaaaacca tcatcaaaat gaaaactgacg tgggtggta tcgtcgccgt gctgctcctg 60  
 acgacctgtc aactcatcac agctgatgac tccagaggta cgccaggagca tcgtgccctg 120  
 aggtcgacca ccaaactccc catgtcact cgctgcaaga gtaaaggagc aaaatgttca 180  
 aggcttatgt atgactgctg cagcggtctc tgcagcaggt actcaggttag atgtggctga 240  
 tccagcgcct gatcttcccc cttctgctgc tctatccttt tctgcctgag tcctccttac 300  
 ctgagagtgg tcatgaacca ctcatcacct actcctctgg aggcccagag gagctacatt 360

gaaataaaag ccgcattgc 379  
 <210> 94  
 <211> 73  
 <212> PRT  
 <213> Conus circumcisus

<400> 94  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg  
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Pro Met Ser Thr Arg Cys Lys Ser  
 35 40 45

Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys Ser Gly Ser  
 50 55 60

Cys Ser Arg Tyr Ser Gly Arg Cys Gly  
 65 70

<210> 95  
 <211> 27  
 <212> PRT  
 <213> Conus circumcisus

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 13 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 95  
 Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Xaa Asp Cys Cys  
 1 5 10 15

Ser Gly Ser Cys Ser Arg Xaa Ser Gly Arg Cys  
 20 25

<210> 96  
 <211> 379  
 <212> DNA  
 <213> Conus circumcisus

<400> 96  
 accaaaaacca tcatcaaaat gaaactgacg tgtgtggta tcgtcgccgt gctgctcctg 60  
 acgacacctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgttccctg 120  
 acgtcgccca ccaaagtctc caagtcgact ggctgcatga aagccggatc ttattgccgc 180  
 tctactacga gaacctgctg cggttattgc gcttatttcg gcaaaaaatg tattgactat 240  
 cccagcaact gatcttcccc ctactgtgct ctatcctttt ctgcctaagt cctccttacc 300  
 tgagagtggt catgaaccac tcatcacccct actccctctgg aggcccagag gagctacatt 360  
 gaaataaaag ccgcattgc 379

<210> 97  
 <211> 77  
 <212> PRT  
 <213> Conus circumcisus

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<400> 97
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr
1          5          10          15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20          25          30
Ser Leu Thr Ser Ala Thr Lys Val Ser Lys Ser Thr Gly Cys Met Lys
35          40          45
Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg Thr Cys Cys Gly Tyr Cys
50          55          60
Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr Pro Ser Asn
65          70          75

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<210> 98
<211> 35
<212> PRT
<213> Conus circumcisus

<220>
<221> PEPTIDE
<222> (1)..(35)
<223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21, 24 and 32
      is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-
      phospho-Ty

<400> 98
Ser Thr Gly Cys Met Lys Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg
1           5           10          15
Thr Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa
20          25          30

Xaa Ser Asn
35

<210> 99
<211> 362
<212> DNA
<213> Conus consors

400> 99
tgaaaactga cgtgtgtgg tgcgtcgcc gtgtgtctcc tgacggcctg tcaactcctc
cagctgatg actccagagg tacgcagaag catcgccccc tgaagtctta caccaaactc
ccatgttaa ctttgcgtg cgcattttac ggaaaacctt gtggatttga caacgactgc
gcaatacat gcgatccagc cagaaagaca tgtacgtagc tgatccggcg tctgatcttc
cccttctgt gctctatcct tttctgcctg agtccctcctt acctgagagt ggtcatgaac
actcatcac ctagtcctc tggaggcttc agaggagcta caatgaaata aaagcgcatt
362

<210> 100
<211> 72
<212> PRT
<213> Conus consors

00> 100

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Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Leu Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Lys Ser Tyr Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala  
 35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Thr Cys  
 50 55 60

Asp Pro Ala Arg Lys Thr Cys Thr  
 65 70

<210> 101

<211> 26

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1  
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 101

Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn  
 1 5 10 15

Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr  
 20 25

<210> 102

<211> 237

<212> DNA

<213> Conus consors

<400> 102

atgaaaactga cgtgtgtgg gatcgctgcc gtcgtgtcc tgacggcctg tcaactcctc 60

acagctgatg actccagagg tacgcagaag catcgccccc tgaggtcgga caccaaactc 120

tccatgtcga ctcgctgaa gggtagcgg aaaccatgca gtaggattgc gtataactgc 180

tgcaccgggtt cttgcagatc aggtaaatgt ggctgatcca ggcgcctgatc tcccccc 237

<210> 103

<211> 71

<212> PRT

<213> Conus consors

<400> 103

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Leu Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly  
 35 40 45

Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser  
 50 55 60

09640082-002230

Cys Arg Ser Gly Lys Cys Gly  
65 70

<210> 104

<211> 25

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Ty  
r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 104

Cys Lys Gly Arg Gly Lys Xaa Cys Ser Arg Ile Ala Xaa Asn Cys Cys  
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
20 25

<210> 105

<211> 320

<212> DNA

<213> Conus consors

<400> 105

atgaaaactga cgtgtgtgg gatcggtcgcc gtgcgtgtcc tgacggcctg tcaactcattc 60

acagctgatg actccaaagg tacgcagaag catcggttccc tgagggtcgac caccaaaatgc 120

tccaaaggcga ctgactgcat tgaagccgga aattatttgcg gacctactgt tatgaaaatc 180

tgctgcggct tttgcagtcc atacagcaaa atatgtatga actatccccaa aaatttgatct 240

tcccccttct gtgctctatc cttttctgcc tgagtcctcc ttacctgaga gtggcatgaa 300

accactcatc acctcgatccc 320

<210> 106

<211> 78

<212> PRT

<213> Conus consors

<400> 106

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Lys Gly Thr Gln Lys His Arg  
20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ala Thr Asp Cys Ile Glu  
35 40 45

Ala Gly Asn Tyr Cys Gly Pro Thr Val Met Lys Ile Cys Cys Gly Phe  
50 55 60

Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn Tyr Pro Gln Asn  
65 70 75

<210> 107

<211> 36

<212> PRT

<213> Conus consors

<220>  
 <221> PEPTIDE  
 <222> (1)..(36)  
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13,  
 25 and 34 is Pro or Hyp; Xaa at residue 10, 26 and 33 is Tyr, 125  
 I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 107  
 Ala Thr Asp Cys Ile Xaa Ala Gly Asn Xaa Cys Gly Xaa Thr Val Met  
 1 5 10 15

Lys Ile Cys Cys Gly Phe Cys Ser Xaa Xaa Ser Lys Ile Cys Met Asn  
 20 25 30

Xaa Xaa Gln Asn  
 35

<210> 108  
 <211> 321  
 <212> DNA  
 <213> Conus consors

<400> 108  
 atgaaaactga cgtgtgtgg gatcgctgcc gtgctgctcc tgacggcctg tcaactcctc 60  
 acagctgatg actccagagg tacgcagaag catcgccccc tgaggtcgga caccaaactc 120  
 tccatgtcga ctcgctgcaa aggtaaagga gcatcatgta caaggcttat gtatgactgc 180  
 tgccacggtt cttgcagcag cagcaagggt agatgtggct gatccggcgc ctgatcttcc 240  
 cccttctgtg ctctatcctt ttctgcctga gtccctccta cctgagaggt ggtcatgaac 300  
 cactcatcac ctgctcccct g 321

<210> 109  
 <211> 73  
 <212> PRT  
 <213> Conus consors

<400> 109  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Leu Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly  
 35 40 45

Lys Gly Ala Ser Cys Thr Arg Leu Met Tyr Asp Cys Cys His Gly Ser  
 50 55 60

Cys Ser Ser Ser Lys Gly Arg Cys Gly  
 65 70

<210> 110  
 <211> 27  
 <212> PRT  
 <213> Conus consors

<220>  
 <221> PEPTIDE

<222> (1)..(27)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 110  
 Cys Lys Gly Lys Gly Ala Ser Cys Thr Arg Leu Met Xaa Asp Cys Cys  
 1 5 10 15  
 His Gly Ser Cys Ser Ser Ser Lys Gly Arg Cys  
 20 25

<210> 111  
 <211> 292  
 <212> DNA  
 <213> Conus consors

<400> 111  
 ggatccatga aactgacgtg catggtgatc gtcggcgtgc tgctcctgac ggccgttcaa 60  
 ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgcctgag gtcggacacc 120  
 aaactctcca tgtcaactcg ctgcaagggt aaaggagcat catgtcatag gacttcgtat 180  
 gactgctgca ccgggtcttg caacagaggt aaatgtggct gatccggcgc ctgatcttcc 240  
 cccttctgtg ctctatcctt ttctgcctga gtcatccata cctgtgctcg ag 292

<210> 112  
 <211> 71  
 <212> PRT  
 <213> Conus consors

<400> 112  
 Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly  
 35 40 45

Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser  
 50 55 60

Cys Asn Arg Gly Lys Cys Gly  
 65 70

<210> 113  
 <211> 25  
 <212> PRT  
 <213> Conus consors

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 113  
 Cys Lys Gly Lys Gly Ala Ser Cys His Arg Thr Ser Xaa Asp Cys Cys  
 1 5 10 15  
 Thr Gly Ser Cys Asn Arg Gly Lys Cys  
 20 25

<210> 114  
 <211> 299  
 <212> DNA  
 <213> Conus consors

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<400> 114  
 gatatccatga aactgacgtg cgtggtgatc gtcggcggtgc tgctccgtac ggcctgtcaa 60  
 ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgcctgaa gtcggacacc 120  
 aaactctcca tgttaacttt gcgcgtcgca tcttacggaa aaccttgtgg tatttacaac 180  
 gactgctgca atacatgcga tccagccaga aagacatgta cgtagctgat ccggcgtctg 240  
 atcttcccccc ttctgtgctc tatccttttc tgctgtgatc atccatacct gtgctcgag 299

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<210> 115  
 <211> 72  
 <212> PRT  
 <213> Conus consors

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<400> 115  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Lys Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala  
 35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Thr Cys  
 50 55 60

Asp Pro Ala Arg Lys Thr Cys Thr  
 65 70

<210> 116  
 <211> 26  
 <212> PRT  
 <213> Conus consors

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<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 and 11 is  
       Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho-  
       spho-Ty

<400> 116  
 Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Xaa Asn Asp Cys Cys Asn  
 1 5 10 15

Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr  
 20 25

<210> 117  
 <211> 434  
 <212> DNA  
 <213> Conus consors

<220>  
 <221> misc\_feature

<222> (1)..(434)  
 <223> n may be any nucleotide

<400> 117  
 ggatccatga aactgacgtg tgtggtgatc gtcggcgtgc tgctcctgac ggcctgtcaa 60  
 ctcatcacag ctgatgactc cagaggtacg cagaagcatac gtgcctgag gtcggacacc 120  
 aaactctcca tgcgtactcg ctgcaagggt acaggaaaac catgcagtag ggttgcgtat 180  
 aactgctgca ccgggttcttg cagatcaggt aaatgtggct gatccagtgc ctgatcttcc 240  
 cccttctgtg ctctatcctt ttctgcctga gtcctcctta cctgagagtg gtcatgaacc 300  
 actcatcacc tgctcctctg gaggcttcag aggagctaca ttgaaataaa agccgcattg 360  
~~caatggaaaaa aannnnnnnn nnnnnnnnn nnnnnnnnn nnnnnnnnn nngaaaaaa~~ 420

aaaaaaaaaaaa aaaa 434

<210> 118  
 <211> 71  
 <212> PRT  
 <213> Conus consors

<400> 118  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly  
 35 40 45

Thr Gly Lys Pro Cys Ser Arg Val Ala Tyr Asn Cys Cys Thr Gly Ser  
 50 55 60

Cys Arg Ser Gly Lys Cys Gly  
 65 70

<210> 119  
 <211> 25  
 <212> PRT  
 <213> Conus consors

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Ty  
 r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 119  
 Cys Lys Gly Thr Gly Lys Xaa Cys Ser Arg Val Ala Xaa Asn Cys Cys  
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
 20 25

<210> 120  
 <211> 393  
 <212> DNA  
 <213> Conus consors

<400> 120

ggatccatga aactgacgtg catggtgatc gtcggcgtgc tgctcctgac ggcctgtcaa 60  
 ctcatcacag ctgatgactc cagaggtacg cagaagcatc gttccctgag gtcgaccacc 120  
 aaagtctcca agtcgactag ctgcatgaaa gccgggtctt attggcgctc tactacgaga 180  
 acctgctgca gttattgcgc ttatttcggc aaattttgta ttgactttcc cagcaactga 240  
 tcttccccct actgtgctct atcctttct gcctctgcct gagtcctcct tacctgagag 300  
 tggcatgaa ccactcatca cctgctcccc tggaggcctc agaggagcta caatgaaata 360  
 aaagccgcat tgcaaaaaaa aaaaaaaaaaaa aaa 393

&lt;210&gt; 121

&lt;211&gt; 77

&lt;212&gt; PRT

&lt;213&gt; Conus consors

<400> 121  
 Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30  
 Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys  
 35 40 45  
 Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg Thr Cys Cys Gly Tyr Cys  
 50 55 60  
 Ala Tyr Phe Gly Lys Phe Cys Ile Asp Phe Pro Ser Asn  
 65 70 75

&lt;210&gt; 122

&lt;211&gt; 35

&lt;212&gt; PRT

&lt;213&gt; Conus consors

<220>  
 <221> PEPTIDE  
 <222> (1)..(35)  
 <223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21 and 24 is  
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos

<400> 122  
 Ser Thr Ser Cys Met Lys Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg  
 1 5 10 15

Thr Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Phe Cys Ile Asp Phe  
 20 25 30

Xaa Ser Asn  
 35

&lt;210&gt; 123

&lt;211&gt; 361

&lt;212&gt; DNA

&lt;213&gt; Conus dalli

&lt;400&gt; 123

accaaaaacca tcatcaaaat gaaactgacg tgtgtggta tcgtcgccgt gctgttcctg

60

acggcctgtc aactcatcac agctgatgac tccagaagta cgccagaagca tcgtgctctg 120  
 aggtcgacca tcaaacactc catgttactg aggagctgca cgcccccgg aggaccttgt 180  
 ggttattata atgactgctg cagtcataa tgcaatataa gcagaaataa atgcgagtag 240  
 ctgatccggc atctgatctt ccccttctgt gctgtccta acctgagagt ggtcatgaac 300  
 catcatcacc tactcctctg gaggcttcag aggagctaca tggaaataaa agccgcattg 360  
 c 361

<210> 124

<211> 73

<212> PRT

<213> Conus dalli

<400> 124  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Ser Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Thr Ile Lys His Ser Met Leu Thr Arg Ser Cys Thr  
 35 40 45

Pro Pro Gly Gly Pro Cys Gly Tyr Tyr Asn Asp Cys Cys Ser His Gln  
 50 55 60

Cys Asn Ile Ser Arg Asn Lys Cys Glu  
 65 70

<210> 125

<211> 28

<212> PRT

<213> Conus dalli

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa at residue 4, 5 and 8 is Pro or Hyp; Xaa at residue 11 and 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 125

Ser Cys Thr Xaa Xaa Gly Gly Xaa Cys Gly Xaa Xaa Asn Asp Cys Cys  
 1 5 10 15

Ser His Gln Cys Asn Ile Ser Arg Asn Lys Cys Xaa  
 20 25

<210> 126

<211> 350

<212> DNA

<213> Conus distans

<400> 126

acccaaaacca tcatcaaaat gaaactgacg tgcgtgttga tcatgccgt gctgttcctg 60

acggcctgtc aactcactag aggaaagctg gagcgtcctg ttctgaggtc gagcgaccaa 120

acctccgggt caacgaagag atgcgaagat cctggtgaac cttgcggaag tgcattcc 180

tgctgcggcg gtagttgcaa ccacaacgtc tgcgcctgaa gctggctgg catctgacca 240

ttcccccttct gtactctatc tctattgcct gagtcatctt tacctgtgag tggcatgaa 300  
 tctctcaata ccttctcccc tggaggcttc agaagaacta gattgaaata 350  
 <210> 127  
 <211> 66  
 <212> PRT  
 <213> Conus distans  
 <400> 127  
 Met Lys Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Thr Arg Gly Lys Leu Glu Arg Pro Val Leu Arg Ser Ser  
 20 25 30  
 Asp Gln Thr Ser Gly Ser Thr Lys Arg Cys Glu Asp Pro Gly Glu Pro  
 35 40 45  
 Cys Gly Ser Asp His Ser Cys Cys Gly Ser Cys Asn His Asn Val  
 50 55 60  
 Cys Ala  
 65  
 <210> 128  
 <211> 25  
 <212> PRT  
 <213> Conus distans  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 2 and 6 is Glu or gamma-carboxy Glu; Xaa at residue 4 and 7 is Pro or Hy  
 <400> 128  
 Cys Xaa Asp Xaa Gly Xaa Xaa Cys Gly Ser Asp His Ser Cys Cys Gly  
 1 5 10 15  
 Gly Ser Cys Asn His Asn Val Cys Ala  
 20 25  
 <210> 129  
 <211> 309  
 <212> DNA  
 <213> Conus ermineus  
 <400> 129  
 atgaaactga cgtgtgtggat gatcgctgccgt tgctgtcc tgacggcctgtcaactcatc  
 acagctgacg actccagacg tacgcagaag catcgccccc tgaggtcgac caccaaacgc  
 gcccacgtcga atcgccccctg caagccgaaa ggacgaaaat gtttccgca tcagaaggac  
 tgctgcaata aaacgtgcac cagatcaaaa tgtccctgat cttccccctt ctgtgctgta  
 tcctttctg cctgagtcct cttacctga gagtggtcag taaccactca tcaccatctc  
 ctctggagg  
 <210> 130  
 <211> 72  
 <212> PRT

<213> Conus ermineus

<400> 130  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg  
 20 25 30  
 Ala Leu Arg Ser Thr Thr Lys Arg Ala Thr Ser Asn Arg Pro Cys Lys  
 35 40 45  
 Pro Lys Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys Cys Asn Lys  
 50 55 60  
 Thr Cys Thr Arg Ser Lys Cys Pro  
 65 70

<210> 131  
 <211> 27  
 <212> PRT  
 <213> Conus ermineus

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 1, 4, 11 and 27 is Pro or Hyp

<400> 131  
 Xaa Xaa Lys Xaa Lys Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys  
 1 5 10 15  
 Cys Asn Lys Thr Cys Thr Arg Ser Lys Cys Xaa  
 20 25

<210> 132  
 <211> 308  
 <212> DNA  
 <213> Conus ermineus

<400> 132  
 aactcatcac agctgatgac tccagaggta cgcaaacga tcgtgccctg aggtcgacca 60  
 ccaaactctc catgctgact cgggcctgct ggtcttccgg aacaccttgt ggtactgata 120  
 gtttatgctg cggtggatgc aatgtatcca aaagtaaatg taactagctg attcggcgtc 180  
 tgaacttccc cttctgtgc tctatcctt tctgcccag tccctccatac ctgagaatgg 240  
 tcatgaacca ctcatcacct actcctctgg agacacctaga agagctacac taaaataaaa 300  
 gcgcttgc 308

<210> 133  
 <211> 54  
 <212> PRT  
 <213> Conus ermineus

<400> 133  
 Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Asn Asp Arg Ala Leu  
 1 5 10 15  
 Arg Ser Thr Thr Lys Leu Ser Met Leu Thr Arg Ala Cys Trp Ser Ser  
 20 25 30

Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys Gly Gly Cys Asn Val  
 35 40 45

Ser Lys Ser Lys Cys Asn  
 50

<210> 134  
 <211> 27  
 <212> PRT  
 <213> Conus ermineus

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at 8 residue is Pro or Hyp; Xaa at residue 3 is Trp or Bromo  
 Tr

<400> 134  
 Ala Cys Xaa Ser Ser Gly Thr Xaa Cys Gly Thr Asp Ser Leu Cys Cys  
 1 5 10 15

Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn  
 20 25

<210> 135  
 <211> 385  
 <212> DNA  
 <213> Conus geographus

<400> 135  
 ggatccatga aactgacgtg cgtggtgatc gtcggcgtgc tgctcctgac ggcctgtcaa 60  
 ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgcctggg gtcgaccacc 120  
 gaactctcct tgtcgactcg ctgcaagtca cccggatctt catgttcacc gactagttat 180  
 aattgctgca ggtcttgcaa tccatacgcc aaaagatgtt acggctaatac cagcgcctga 240  
 tcttccccct tctgtgctct atcccttcct gtctgagtc tcccttacctg agagtggtca 300  
 tgaaccactc ctcacctact tctctggagg ctccggagga gctacattga aataaaagcc 360  
 gcattgtaaa aaaaaaaaaaaaaaa 385

<210> 136  
 <211> 73  
 <212> PRT  
 <213> Conus geographus

<400> 136  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Gly Ser Thr Thr Glu Leu Ser Leu Ser Thr Arg Cys Lys Ser  
 35 40 45

Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys  
 50 55 60

Asn Pro Tyr Ala Lys Arg Cys Tyr Gly  
 65 70

PROTEIN SEQUENCES

<210> 137  
 <211> 27  
 <212> PRT  
 <213> Conus geographus

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13, 22  
 and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
 or O-phospho-Ty

<400> 137  
 Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys  
 1 5 10 15

Arg-Ser-Cys-Asn-Xaa-Xaa-Ala-Lys-Arg-Cys-Xaa  
 20 25

<210> 138  
 <211> 396  
 <212> DNA  
 <213> Conus geographus

<400> 138  
 ggatccatga aactgacgtg tgtggtgatc gtcggcgtgc tgctcctgac ggccctgtcaa 60  
 ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgcctgag gtcgtccacc 120  
 aaactcacct tgcgactcg ctgcaaatac cccggaaactc catgttcaag gggtatgcgt 180  
 gattgctgca cgccttgctt gttatacagc aacaaatgta ggctacta acccagcgcc 240  
 tgcattccc cttctgtgc tctattcctt tctgcctgag tcctccttac ctgaaagtgg 300  
 tcatgaacca ctcatcacct acttctctgg aggcttcaga agagctacat tgaataaaaa 360  
 gccgcattgc aatgacaaaa aaaaaaaaaa aaaaaa 396

<210> 139  
 <211> 74  
 <212> PRT  
 <213> Conus geographus

<400> 139  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Ser Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser  
 35 40 45

Pro Gly Thr Pro Cys Ser Arg Gly Met Arg Asp Cys Cys Thr Pro Cys  
 50 55 60

Leu Leu Tyr Ser Asn Lys Cys Arg Arg Tyr  
 65 70

<210> 140  
 <211> 29  
 <212> PRT  
 <213> Conus geographus

<220>  
 <221> PEPTIDE  
 <222> (1)..(29)  
 <223> Xaa at residue 4, 7 and 18 is Pro or Hyp; Xaa at residue 22 and 29 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 140  
 Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys  
 1 5 10 15

Thr Xaa Cys Leu Leu Xaa Ser Asn Lys Cys Arg Arg Xaa  
 20 25

<210> 141  
 <211> 407  
 <212> DNA  
 <213> Conus geographus

<400> 141  
 ggaattccgt ttctgcgtg cttccttgg catcaccaaa accatcatca aaatgaaact 60  
 gacgtgtgtg gtgatcgctg ccgtgctgct cctgacggcc tgtcaactca tcacagctga 120  
 tgactccaga ggtacgcaga agcatcgatgc cctgggtcg accaccgaac ttccttgc 180  
 gactcgctgc aagtccacccg gatcttcatg ttcaccgact agttataatt gctgcaggc 240  
 ttgcaatcca tacaccaaaa gatgttacgg ctaatccagc gcctgatctt ccctgctctg 300  
 agtcctcctt acctgagagt ggtcatgaac cactcatcac ctacttctct aggccggtcg 360  
 gagggagctac attgaaataa aagccgcatt gaaaaaaaaaaaaaaa 407

<210> 142  
 <211> 73  
 <212> PRT  
 <213> Conus geographus

<400> 142  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Gly Ser Thr Thr Glu Leu Ser Leu Ser Thr Arg Cys Lys Ser  
 35 40 45

Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys  
 50 55 60

Asn Pro Tyr Thr Lys Arg Cys Tyr Gly  
 65 70

<210> 143  
 <211> 27  
 <212> PRT  
 <213> Conus geographus

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13, 22 and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr

or O-phospho-Ty

<400> 143

Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys  
 1 5 10 15

Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys Xaa  
 20 25

<210> 144

<211> 28

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13, 22  
 and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
 or O-phospho-Ty

<400> 144

Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys  
 1 5 10 15

Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys Xaa Gly  
 20 25

<210> 145

<211> 26

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13 and  
 22 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or  
 O-phospho-Ty

<400> 145

Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys  
 1 5 10 15

Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys  
 20 25

<210> 146

<211> 314

<212> DNA

<213> Conus geographus

<400> 146

catcacagct gatgactcca gaggtacgca gaagcatcggt gccctgaggt cgtccaccaa

60

actcaccttg tcgactcgct gcaaattcacc cggaaactcca tggtaaagggtatgcgtga

120

ttgctgcacg tcttgctgt tatacagcaa caaatgtagg cgctactaac ccagcgcctg

180

atcttccccc ttctgtgctc tattcctttc tgcctgagtc ctccttaccc gaaagtggtc

240

atgaaccact catcacctac ttctctggag gcttcagaag agctacattg aaataaaagc

300

cgcattgcaa tgac

314

<210> 147  
 <211> 55  
 <212> PRT  
 <213> Conus geographus

<400> 147  
 Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg Ala Leu Arg  
 1 5 10 15  
 Ser Ser Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser Pro Gly Thr  
 20 25 30  
 Pro Cys Ser Arg Gly Met Arg Asp Cys Cys Thr Ser Cys Leu Leu Tyr  
 35 40 45  
 Ser Asn Lys Cys Arg Arg Tyr  
 5.0 55

<210> 148  
 <211> 29  
 <212> PRT  
 <213> Conus geographus

<220>  
 <221> PEPTIDE  
 <222> (1)..(29)  
 <223> Xaa at residue 4 and 7 is Pro or Hyp; Xaa at residue 22 and 29 is  
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho  
 spho-Ty

<400> 148  
 Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys  
 1 5 10 15  
 Thr Ser Cys Leu Leu Xaa Ser Asn Lys Cys Arg Arg Xaa  
 20 25

<210> 149  
 <211> 29  
 <212> PRT  
 <213> Conus geographus

<220>  
 <221> PEPTIDE  
 <222> (1)..(29)  
 <223> Xaa at residue 4 and 7 is Pro or Hyp; Xaa at residue 22 and 29 is  
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho  
 spho-Ty

<400> 149  
 Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys  
 1 5 10 15  
 Thr Ser Cys Leu Ser Xaa Ser Asn Lys Cys Arg Arg Xaa  
 20 25

<210> 150  
 <211> 380  
 <212> DNA  
 <213> Conus laterculatus

<400> 150  
 accaaaaacca tcataaaaaat gaaactgacg tgggtggta tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac cgctgatgac tccagaggta cgccagaagca tcgtgccctg 120

aggtcgacca ccaatctctc catgctgact cggaagtgct ggccttccgg aagctattgt 180  
 cgtgcgaata gttaaatgctg cagtggatgc gatcggaaaca gaaataaaatg ttactagctg 240  
 attcggcgtc tgaacttcct ccttctgtgc tctatcctt tctgcccag tcctccatac 300  
 ctgagagtgg tcatgaacca ctcaactcct actcctctgg aggcctcaga agagctacat 360  
 taaaaataaaa gccgcattgc 380

<210> 151  
 <211> 72  
 <212> PRT  
 <213> Conus laterculatus

<400> 151  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Leu Thr Arg Lys Cys Trp  
 35 40 45

Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys Ser Gly Cys  
 50 55 60

Asp Arg Asn Arg Asn Lys Cys Tyr  
 65 70

<210> 152  
 <211> 27  
 <212> PRT  
 <213> Conus laterculatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 4 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo  
 Trp; Xaa at residue 8 and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-  
 iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 152  
 Lys Cys Xaa Xaa Ser Gly Ser Xaa Cys Arg Ala Asn Ser Lys Cys Cys  
 1 5 10 15

Ser Gly Cys Asp Arg Asn Arg Asn Lys Cys Xaa  
 20 25

<210> 153  
 <211> 367  
 <212> DNA  
 <213> Conus laterculatus

<400> 153  
 accaaaaaccca tcataaaaaat gaaactgacg tgggtggta tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac agctgatgac tccagaggta cgccagaagca tcgtgcctcg 120  
 aggtcgacca ccaactctc catatcgact cgctgccttc ctccggatc atattgtaa 180  
 gcgacaacgg aagtctgctg ctcttcttgc cttcaattcg ctcagatatg ttcgggttga 240

tcttcctct tctgtgctct atcctttct gcctgagtc tccatacctg agaatggta 300  
 tgaaccactc aacatctact cctctggagg cctcagaaga gctatattga aataaaagcc 360  
 gcattgc 367  
 <210> 154  
 <211> 73  
 <212> PRT  
 <213> Conus laterculatus

<400> 154  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

---

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Ile Ser Thr Arg Cys Leu Pro  
 35 40 45

Pro Gly Ser Tyr Cys Lys Ala Thr Thr Glu Val Cys Cys Ser Ser Cys  
 50 55 60

Leu Gln Phe Ala Gln Ile Cys Ser Gly  
 65 70

<210> 155  
 <211> 27  
 <212> PRT  
 <213> Conus laterculatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 13 is Glu or gamma-carboxy Glu; Xaa at residue 3 and 4 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 155  
 Cys Leu Xaa Xaa Gly Ser Xaa Cys Lys Ala Thr Thr Xaa Val Cys Cys  
 1 5 10 15

Ser Ser Cys Leu Gln Phe Ala Gln Ile Cys Ser  
 20 25

<210> 156  
 <211> 373  
 <212> DNA  
 <213> Conus laterculatus

<400> 156  
 accaaaaacca tcatcaaaat gaaactgacg tgtgtggta tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac agctgatgac tccagaggta cgccagaagca tcgtgccctg 120  
 aggtcgacca ccaatctctc catgtcgact cgctgcaagt ctcccggatc atcatgttagc 180  
 gtgtctatgc gtaactgctg cacttctgc aattcacgca ccaagaaaatg tacgcgacgt 240  
 ggctgaactt cccccttctg tgctctatcc ttttctgccc gagtcctcca tacctgagag 300  
 tggcatgaa ccactcaaca tctactcctc tggaggcctc agaagagcta tattgaaata 360  
 aaagccgcat tgc 373

<210> 157  
 <211> 75  
 <212> PRT  
 <213> Conus laterculatus

<400> 157  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Ser Thr Arg Cys Lys Ser  
 35 40 45

Pro Gly Ser Ser Cys Ser Val Ser Met Arg Asn Cys Cys Thr Ser Cys  
 50 55 60

Asn Ser Arg Thr Lys Lys Cys Thr Arg Arg Gly  
 65 70 75

<210> 158  
 <211> 29  
 <212> PRT  
 <213> Conus laterculatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(29)  
 <223> Xaa at residue 3 is Pro or Hyp

<400> 158  
 Cys Lys Ser Xaa Gly Ser Ser Cys Ser Val Ser Met Arg Asn Cys Cys  
 1 5 10 15

Thr Ser Cys Asn Ser Arg Thr Lys Lys Cys Thr Arg Arg  
 20 25

<210> 159  
 <211> 330  
 <212> DNA  
 <213> Conus laterculatus

<400> 159  
 accaaaaacca tcatcaaaat gaaactgacg tgggtggta tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120  
 aggtcgacaa ccaaactctc catgctgact cggacctgct ggccttccgg aacagcttgt 180  
 ggtattgata gtaactgctg cagtggatgc aatgtatcca gaagtaaatg taactagctg 240  
 attcggcgtc taaacttcct ccttctgcct gagtcctcca tacctgagag tggcatgaa 300  
 ccacatcatc acctcatctc tggaggcctc 330

<210> 160  
 <211> 72  
 <212> PRT  
 <213> Conus laterculatus

<400> 160  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Leu Thr Arg Thr Cys Trp  
 35 40 45

Pro Ser Gly Thr Ala Cys Gly Ile Asp Ser Asn Cys Cys Ser Gly Cys  
 50 55 60

Asn Val Ser Arg Ser Lys Cys Asn  
 65 70

<210> 161  
 <211> 27  
 <212> PRT

<213> Conus laterculatus

<220>

<221> PEPTIDE  
 <222> (1)...(27)

<223> Xaa at residue 4 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo  
 Tr

<400> 161

Thr Cys Xaa Xaa Ser Gly Thr Ala Cys Gly Ile Asp Ser Asn Cys Cys  
 1 5 10 15

Ser Gly Cys Asn Val Ser Arg Ser Lys Cys Asn  
 20 25

<210> 162

<211> 363

<212> DNA

<213> Conus laterculatus

<400> 162

acccaaaacca tcataaaaaat gaaaactgacg tgggtggta tcgtcgccgt gctgctcctg 60

acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120

aggtcgacca ccaatctctc catgctgact cgaaagtgct ggccttccgg aagctattgt 180

cgtgcgata gttaatgctg cagtggatgc gatcggaaaca gaagtaatg taactagctg 240

attcggcggtc taaacttcct cttctgcct gagtcctcca tacctgagag tggcatgaa 300

ccactcatca cttactcctc tggaggcctc aaaggagcta cattgaaata aaagccgcat 360

tgc 363

<210> 163

<211> 72

<212> PRT

<213> Conus laterculatus

<400> 163

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Leu Thr Arg Lys Cys Trp  
 35 40 45

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Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys Ser Gly Cys  
 50 55 60

Asp Arg Asn Arg Ser Lys Cys Asn  
 65 70

<210> 164

<211> 27

<212> PRT

<213> Conus laterculatus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 4 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo  
 Trp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Ty  
 r, O-sulpho-Tyr or O-phospho-Ty

<400> 164

Lys Cys Xaa Xaa Ser Gly Ser Xaa Cys Arg Ala Asn Ser Lys Cys Cys  
 1 5 10 15

Ser Gly Cys Asp Arg Asn Arg Ser Lys Cys Asn  
 20 25

<210> 165

<211> 391

<212> DNA

<213> Conus leopardus

<220>

<221> misc\_feature

<222> (1)..(391)

<223> n may be any nucleotide

<400> 165

atgaaaactga cgtgtgtggatcgtagct gtgtgtttcc tgacggcctg tcaactcact  
 acagctgaca tctccagagg tacgcggaaag cgtcgtgctc tgaggtcgac caccaaactc  
 tccaggtcgc tcttgagtg cgcccttcc ggtggacgtt gtggtttttt aaagtccctgc  
 tgcaaggat attgcgatgg ggaaagcact tcatgtgtga gtggccata cagcatctga  
 tcttcccgcc ttcaagtgc ttccttttc tgcctgagtc ctccataacct ctgagcggtc  
 atgaaccact caacacctac tcctctggag gcttcaggaa actatattaa aataaagccg  
 cattgcaacg aaanaaaaaaa aaaaaaaaaa a 60  
 391

<210> 166

<211> 79

<212> PRT

<213> Conus leopardus

<400> 166

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Arg Lys Arg Arg  
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Ser Leu Phe Glu Cys Ala  
 35 40 45

Pro Ser Gly Gly Arg Cys Gly Phe Leu Lys Ser Cys Cys Glu Gly Tyr  
 50 55 60

Cys Asp Gly Glu Ser Thr Ser Cys Val Ser Gly Pro Tyr Ser Ile  
 65 70 75

<210> 167

<211> 37

<212> PRT

<213> Conus leopardus

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residue 4, 20 and 26 is Glu or gamma-carboxy Glu; Xaa at residue 7 and 34 is Pro or Hyp; Xaa at residue 22 and 35 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 167

Ser Leu Phe Xaa Cys Ala Xaa Ser Gly Gly Arg Cys Gly Phe Leu Lys  
 1 5 10 15

Ser Cys Cys Xaa Gly Xaa Cys Asp Gly Xaa Ser Thr Ser Cys Val Ser  
 20 25 30

Gly Xaa Xaa Ser Ile  
 35

<210> 168

<211> 365

<212> DNA

<213> Conus leopardus

<400> 168

atgaaaactga cgtgtgtgg gatcgtcgct gtgctgttcc tgacggcctg tcaactcact 60

acagctgaca tctccagagg tacgtgaaag catcgtggtg tgggtcgac caccggactc 120

tccccgtggc cttggactg cacggctccc agtcaacctt gtggttattt tcctaggtgc 180

tgtggacatt gcgatgtacg cagggtatgt acgagtggct gatccggcgt ctgatcttc 240

cgccttctgt gctgtatcct tttctgcctg agtcctccat acccgtgagt ggtcatgaac 300

cactcaacac ctactcctct ggaggcttca gaggaactat attaaaataa agccgcattg 360

caatg 365

<210> 169

<211> 73

<212> PRT

<213> Conus leopardus

<400> 169

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Trp Lys His Arg  
 20 25 30

Gly Val Gly Ser Thr Thr Gly Leu Ser Pro Trp Pro Leu Asp Cys Thr  
 35 40 45

Ala Pro Ser Gln Pro Cys Gly Tyr Phe Pro Arg Cys Cys Gly His Cys  
 50 55 60

Asp Val Arg Arg Val Cys Thr Ser Gly  
 65 70

<210> 170  
 <211> 30  
 <212> PRT  
 <213> Conus leopardus

<220>  
 <221> PEPTIDE  
 <222> (1)..(30)  
 <223> Xaa at residue 2, 8, 11 and 16 is Pro or Hyp; Xaa at residue 1 is  
 Trp or Bromo Trp; Xaa at residue 14 is Tyr, 125I-Tyr, mono-iodo-  
 Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 170  
 Xaa Xaa Leu Asp Cys Thr Ala Xaa Ser Gln Xaa Cys Gly Xaa Phe Xaa  
 1 5 10 15

Arg Cys Cys Gly His Cys Asp Val Arg Arg Val Cys Thr Ser  
 20 25 30

<210> 171  
 <211> 381  
 <212> DNA  
 <213> Conus leopardus

<400> 171  
 atgaaaactga cgtgtgtgg gatcgctcgat gtgctgttcc tgacggcctg tcaactca  
 acagctgaca tctccagagg tacgcggaaag catcgatcgatc tgaggtcgac caccaaactc  
 tccaggtcgatc cctcttaggtg catgtctccc ggtggaaattt gtgggtgattt tggtgactgc  
 tgcgaaattt gcaatgtgta cggtatatgt gtgagtgact taccggcat ctgatcttc  
 cgccattctgt gctctatcct tttctgcctg agtcctccat acccctgagt ggtcatggac  
 cactcaacac ctactcctct ggaggcttca gaggaactac attaaaataa agccgcattt  
 caaaaaaaaaaaaaaaa aaaaaaaaaa a 381

<210> 172  
 <211> 77  
 <212> PRT  
 <213> Conus leopardus

<400> 172  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Arg Lys His Arg  
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Ser Pro Ser Arg Cys Met  
 35 40 45

Ser Pro Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Glu Ile Cys  
 50 55 60

Asn Val Tyr Gly Ile Cys Val Ser Asp Leu Pro Gly Ile  
 65 70 75

PROTEIN SEQUENCES

<210> 173  
 <211> 31  
 <212> PRT  
 <213> Conus leopardus

<220>  
 <221> PEPTIDE  
 <222> (1)..(31)  
 <223> Xaa at residue 16 is Glu or gamma-carboxy Glu; Xaa at residue 4 and 29 is Pro or Hyp; Xaa at residue 21 is Tyr, 125I-Tyr, mono-iod o-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 173  
 Cys Met Ser Xaa Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Xaa  
 1 5 10 15

---

Ile Cys Asn Val Xaa Gly Ile Cys Val Ser Asp Leu Xaa Gly Ile  
 20 25 30

<210> 174  
 <211> 404  
 <212> DNA  
 <213> Conus leopardus

<400> 174  
 atgaaaactga cgtgtgtggatgcgtcgct gtgctgttcc tgacggcctgtcaactcact 60  
 acagctgatg attccagagg tacacgaaag catcgctc tgaggtcaac caccggaaactc  
 tccaggtggcccgaggactg cgccctccc ggtggagctt gtgggttttt tgatcactgc 120  
 tgcggatatt gcgaaacgtt ttacaatacg ttagatgatggatggctgatccggcgcttga 180  
 tctttccgccc ttctgttgct ctatctttt ctgcctgagt cctccatac cccgttgagt 240  
 ggtccatgaa ccactccaaac acctactccc tccttggaaag cttccaaagg aaacgacatt 300  
 taaaataaaat tccccattgc aattggaaaa aaaaaaaaaa aaaa 360  
 404

<210> 175  
 <211> 72  
 <212> PRT  
 <213> Conus leopardus

<400> 175  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

---

Cys Gln Leu Thr Thr Ala Asp Asp Ser Arg Gly Thr Arg Lys His Arg  
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Trp Pro Arg Tyr Cys Ala  
 35 40 45

Pro Pro Gly Gly Ala Cys Gly Phe Phe Asp His Cys Cys Gly Tyr Cys  
 50 55 60

Glu Thr Phe Tyr Asn Thr Cys Arg  
 65 70

<210> 176  
 <211> 27  
 <212> PRT  
 <213> Conus leopardus

TOP SECRET

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 20 is Glu or gamma-carboxy Glu; Xaa at residue 4 a  
       nd 5 is Pro or Hyp; Xaa at residue 1, 18 and 23 is Tyr, 125I-Tyr,  
       mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 176  
 Xaa Cys Ala Xaa Xaa Gly Gly Ala Cys Gly Phe Phe Asp His Cys Cys  
 1                  5                  10                  15  
  
 Gly Xaa Cys Xaa Thr Phe Xaa Asn Thr Cys Arg  
 20                  25

<210> 177  
 <211> 292  
 <212> DNA  
 <213> Conus lynceus

<400> 177  
 atgaaaactga cgtgtgtgg gatcgctgcc gtcgtgtcc tgacggcctg tcaactcatc   60  
  
 acagctgatg actccagacg tacacagaag catcgctgcc tgaggtcgac caccaatctc   120  
  
 tccatgtcga ctcgctgcaa gtctcccgga tcaccatgta gtgtgacatc gtataactgc   180  
  
 tgcactttt gctttcata cactaagaaa tgtcgggcct ctatgtAAC cactcatcac   240  
  
 ctactcctct ggaggcctca gaagagctac actgaaataa aagccgcatt gg       292

<210> 178  
 <211> 75  
 <212> PRT  
 <213> Conus lynceus

<400> 178  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1                  5                  10                  15  
  
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg  
 20                  25                  30

Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Ser Thr Arg Cys Lys Ser  
 35                  40                  45

Pro Gly Ser Pro Cys Ser Val Thr Ser Tyr Asn Cys Cys Thr Phe Cys  
 50                  55                  60

Ser Ser Tyr Thr Lys Lys Cys Arg Ala Ser Leu  
 65                  70                  75

<210> 179  
 <211> 30  
 <212> PRT  
 <213> Conus lynceus

<220>  
 <221> PEPTIDE  
 <222> (1)..(30)  
 <223> Xaa at residue 4 and 7 is Pro or Hyp; Xaa at residue 13 and 22 is  
       Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho  
       spho-Ty

<400> 179

Cys Lys Ser Xaa Gly Ser Xaa Cys Ser Val Thr Ser Xaa Asn Cys Cys  
 1 5 10 15

Thr Phe Cys Ser Ser Xaa Thr Lys Lys Cys Arg Ala Ser Leu  
 20 25 30

<210> 180

<211> 355

<212> DNA

<213> Conus lynceus

<400> 180

atgaaactga cgtgtgtgg gatcgctgcc gtgctgctcc tgacggcctg tcaactcatc  
 acagctgatg actccagagg tacgcagaag catcggtgcc tgagggtcgac caccaaacta  
 tccatgtata-ctcgctgycgc aggtccagga gcaatttgc ctaatagggt atgctgcgg  
 tattgcagta aaagaacaca tctatgtcat tcgcgaactg gctgatcttc ccccttctgt  
 gctctatcct ttttctgcct gagtcctcca tacctgagaa tggtcatgaa ccactcatca  
 cctactcctc ttggagacct cagaggagct acactgaaat aaaagccgca ttggc

60

120

180  
 gctctatcct ttttctgcct gagtcctcca tacctgagaa tggtcatgaa ccactcatca  
 240  
 cctactcctc ttggagacct cagaggagct acactgaaat aaaagccgca ttggc  
 300  
 355

<210> 181

<211> 74

<212> PRT

<213> Conus lynceus

<400> 181

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Tyr Thr Arg Cys Ala Gly  
 35 40 45

Pro Gly Ala Ile Cys Pro Asn Arg Val Cys Cys Gly Tyr Cys Ser Lys  
 50 55 60

Arg Thr His Leu Cys His Ser Arg Thr Gly  
 65 70

<210> 182

<211> 28

<212> PRT

<213> Conus lynceus

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue 16 is Tyr, 1  
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 182

Cys Ala Gly Xaa Gly Ala Ile Cys Xaa Asn Arg Val Cys Cys Gly Xaa  
 1 5 10 15

Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr  
 20 25





aggattgcgt ataactgctg caccgggtctc tgcatcgatcgatgtgg ctgatccagt 240  
 gcctgatctt ccccccgttctg tgctctatcc tttttctgcc tgagtccctcc ttacctgaga 300  
 gtggtcatga accactca  
 318

<210> 190  
 <211> 71  
 <212> PRT  
 <213> Conus magus

<400> 190  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys-Gln-Leu-Ile-Thr-Ala-Asp-Asp-Ser-Arg-Gly-Thr-Gln-Lys-His-Arg  
 20 25 30

Ala-Leu-Arg-Ser-Asp-Thr-Lys-Leu-Ser-Met-Ser-Thr-Arg-Cys-Lys-Gly  
 35 40 45

Thr-Gly-Lys-Pro-Cys-Ser-Arg-Ile-Ala-Tyr-Asn-Cys-Cys-Thr-Gly-Ser  
 50 55 60

Cys-Arg-Ser-Gly-Lys-Cys-Gly  
 65 70

<210> 191  
 <211> 25  
 <212> PRT  
 <213> Conus magus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Ty  
 r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 191  
 Cys-Lys-Gly-Thr-Gly-Lys-Xaa-Cys-Ser-Arg-Ile-Ala-Xaa-Asn-Cys-Cys  
 1 5 10 15

Thr-Gly-Ser-Cys-Arg-Ser-Gly-Lys-Cys  
 20 25

<210> 192  
 <211> 259  
 <212> DNA  
 <213> Conus magus

<400> 192  
 accaaaaacca tcataaaaaat gaaaactgacg tgggtggta tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg  
 aagtccggaca ccaaactctc catgttaact ttgcgctgca catcttacgg aaaaccttgt 120  
 ggtatattaca acgactgctg caatacatgc gatccagcca gaaagacatg tacgttagctg 180  
 atccggcgctc tggatcttcc 240  
 259

<210> 193  
 <211> 72  
 <212> PRT

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<213> Conus magus

<400> 193

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ala Leu Lys Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala  
35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Thr Cys  
50 55 60

Asp Pro Ala Arg Lys Thr Cys Thr  
65 70

<210> 194

<211> 26

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 and 11 is  
Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho-  
spho-Ty

<400> 194

Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Xaa Asn Asp Cys Cys Asn  
1 5 10 15

Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr  
20 25

<210> 195

<211> 254

<212> DNA

<213> Conus magus

<400> 195

gaattttcag catcaccaaa accatcatca aaatgaaaact gacgtgtgtg gtgatcgtcg 60

ccgtgctgct cctgacggcc tgtcaactca tcacagctga tgactccaga ggtacgcaga 120

agcatcgtgc cctgaggctcg gacacccaaac tctccatgtc aactcgctgc aagggtaaag 180

gagcatcatg tcataggact tcgtatgact gctgcaccgg ttcttgcaac agaggtaaat 240

ttggctgatc cgcc 254

<210> 196

<211> 71

<212> PRT

<213> Conus magus

<400> 196

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly  
 35 40 45

Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser  
 50 55 60

Cys Asn Arg Gly Lys Phe Gly  
 65 70

<210> 197

<211> 25

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)-(25)

<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, o-sulpho-Tyr or O-phospho-Tyr

<400> 197

Cys Lys Gly Lys Gly Ala Ser Cys His Arg Thr Ser Xaa Asp Cys Cys  
 1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Lys Cys  
 20 25

<210> 198

<211> 358

<212> DNA

<213> Conus miles

<400> 198

ggatccatga aactgacgtg cgtggtgatc atcgccatgc tgttcctgac agcctatcaa 60

ctcgctacag ctgcgagcta cgccaaaggt aaacagaagc atcgtgctct gagggcagct 120

gacaaacacc tcaggttgc acaggcgtgc aatgatcgcg gtggaggtt cagtcacat 180

cctcactgct gcgggtggAAC ttgcaataag cttattggcg tatgtctgta aagctggct 240

gccgtctgat attcccttgc tgtgcttcat cctctttgc ctgagtcatc catacctgtg 300

aatggtaag agccactcaa tacctattcc tctggggct tcagaggaac tactttac 358

<210> 199

<211> 74

<212> PRT

<213> Conus miles

<400> 199

Met Lys Leu Thr Cys Val Val Ile Ile Ala Met Leu Phe Leu Thr Ala  
 1 5 10 15

Tyr Gln Leu Ala Thr Ala Ala Ser Tyr Ala Lys Gly Lys Gln Lys His  
 20 25 30

Arg Ala Leu Arg Pro Ala Asp Lys His Leu Arg Leu Thr Lys Arg Cys  
 35 40 45

Asn Asp Arg Gly Gly Cys Ser Gln His Pro His Cys Cys Gly Gly  
 50 55 60

Thr Cys Asn Lys Leu Ile Gly Val Cys Leu  
 65 70

<210> 200  
 <211> 27  
 <212> PRT  
 <213> Conus arenatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 12 is Pro or Hyp

<400> 200  
 Cys Asn Asp Arg Gly Gly Gly Cys Ser Gln His Xaa His Cys Cys Gly  
 1 5 10 15

Gly Thr Cys Asn Lys Leu Ile Gly Val Cys Leu  
 20 25

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<210> 201  
 <211> 292  
 <212> DNA  
 <213> Conus monachus

<400> 201  
 accaaaaacca tcataaaaaat gaaactgacg agtgtggta tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac agctgatgac tccagaggtt cgcagaagca tcgtgccctg 120  
 aggtcggaca ccaaactctc catatcgact cgctgcaagt ctacaggaaa atcatgcagt 180  
 aggattgcgt ataactgctg caccggttct tgcagatcag gttaatgtgg ctgatccagc 240  
 gcctgatctt ccccttctg tgctctatcc ttttctgcct gagtcctcct ta 292

<210> 202  
 <211> 71  
 <212> PRT  
 <213> Conus monachus

<400> 202  
 Met Lys Leu Thr Ser Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Ile Ser Thr Arg Cys Lys Ser  
 35 40 45

Thr Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser  
 50 55 60

Cys Arg Ser Gly Lys Cys Gly  
 65 70

<210> 203  
 <211> 25  
 <212> PRT  
 <213> Conus monachus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

&lt;400&gt; 203

Cys	Lys	Ser	Thr	Gly	Lys	Ser	Cys	Ser	Arg	Ile	Ala	Xaa	Asn	Cys	Cys
1				5					10					15	

Thr	Gly	Ser	Cys	Arg	Ser	Gly	Lys	Cys	
				20				25	

&lt;210&gt; 204

&lt;211&gt; 258

&lt;212&gt; DNA

&lt;213&gt; Conus monachus

&lt;400&gt; 204

acccaaaacca	tcatcaaaaat	gaaaactgacg	agtgtggta	tcgtcgccgt	gctgctcctg	60
-------------	-------------	-------------	-----------	------------	------------	----

acggccctgtc	aactcatcac	agctgatgac	tccagaggta	cgcagaagca	tcgtgcccgt	120
-------------	------------	------------	------------	------------	------------	-----

aggtcggaca	ccaacctctc	catgtcgact	cgctgcaagg	gtaaaggatc	ttcatgttagt	180
------------	------------	------------	------------	------------	-------------	-----

aggaccatgt	ataactgctg	caccggttct	tgcaacagag	gtaaatgtgg	ctgatccagc	240
------------	------------	------------	------------	------------	------------	-----

gcctgatctt	cccccttc					258
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&lt;210&gt; 205

&lt;211&gt; 71

&lt;212&gt; PRT

&lt;213&gt; Conus monachus

&lt;400&gt; 205

Met	Lys	Leu	Thr	Ser	Val	Val	Ile	Val	Ala	Val	Leu	Leu	Leu	Thr	Ala
1				5					10					15	

Cys	Gln	Leu	Ile	Thr	Ala	Asp	Asp	Ser	Arg	Gly	Thr	Gln	Lys	His	Arg
				20				25				30			

Ala	Leu	Arg	Ser	Asp	Thr	Asn	Leu	Ser	Met	Ser	Thr	Arg	Cys	Lys	Gly
		35				40					45				

Lys	Gly	Ser	Ser	Cys	Ser	Arg	Thr	Met	Tyr	Asn	Cys	Cys	Thr	Gly	Ser
50				55						60					

Cys	Asn	Arg	Gly	Lys	Cys	Gly
65				70		

&lt;210&gt; 206

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Conus monachus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(25)

&lt;223&gt; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

&lt;400&gt; 206

Cys	Lys	Gly	Lys	Gly	Ser	Ser	Cys	Ser	Arg	Thr	Met	Xaa	Asn	Cys	Cys
1				5					10					15	

Thr	Gly	Ser	Cys	Asn	Arg	Gly	Lys	Cys	
				20				25	

&lt;210&gt; 207

&lt;211&gt; 258

<212> DNA  
 <213> Conus obscurus

<400> 207  
 ctctctctct ctctgctgga caggtcgccct ccctgcatga aaggcggatc gtcatgccgc 60  
 ggtactacgg gagtctgttg cggttttgc agtgatttcg gctataaaatg tagggactat 120  
 ccccaaaact gatcttcccc cttctgtgct ctatcctttt ctgtccgagt cctcctgacc 180  
 tgagagtggt catgaaccac tcatcaccta cccctctggg gcttcacagg atctacattg 240  
 aaataaaaagc cgcatattgc 258

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<210> 208  
 <211> 39  
 <212> PRT  
 <213> Conus obscurus

<400> 208  
 Leu Leu Asp Arg Ser Pro Pro Cys Met Lys Gly Gly Ser Ser Cys Arg  
 1 5 10 15

Gly Thr Thr Gly Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Tyr Lys  
 20 25 30

Cys Arg Asp Tyr Pro Gln Asn  
 35

<210> 209  
 <211> 35  
 <212> PRT  
 <213> Conus obscurus

<220>  
 <221> PEPTIDE  
 <222> (1)..(35)  
 <223> Xaa at residue 2, 3 and 33 is Pro or Hyp; Xaa at residue 27 and 3  
 2 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O  
 -phospho-Ty

<400> 209  
 Ser Xaa Xaa Cys Met Lys Gly Gly Ser Ser Cys Arg Gly Thr Thr Gly  
 1 5 10 15

Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Xaa Lys Cys Arg Asp Xaa  
 20 25 30

Xaa Gln Asn  
 35

<210> 210  
 <211> 259  
 <212> DNA  
 <213> Conus obscurus

<400> 210  
 ctctctctct ctctgctgga caggtcgact cgctgcttgc ctgacggaac gtcttgcctt 60  
 ttttagtagga tcagatgctg cggtacttgc agttcaatct taaagtcatg tgtgagctga 120  
 tccagcggtt gatcttcctc cctctgtgct ccattctttt ctgcctgagt tctccttacc 180  
 tgagagtggt catgaaccac tcacatcaccta ctcttctggaa ggcttcagag gagctacatt 240

gaaataaaag ccgcattgc

259

&lt;210&gt; 211

&lt;211&gt; 32

&lt;212&gt; PRT

&lt;213&gt; Conus obscurus

&lt;400&gt; 211

Arg Ser Thr Arg Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg  
1 5 10 15Ile Arg Cys Cys Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser  
20 25 30

&lt;210&gt; 212

&lt;211&gt; 28

&lt;212&gt; PRT

&lt;213&gt; Conus monachus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(28)

&lt;223&gt; Xaa at residue 3 is Pro or Hyp

&lt;400&gt; 212

Cys Leu Xaa Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys  
1 5 10 15Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser  
20 25

&lt;210&gt; 213

&lt;211&gt; 330

&lt;212&gt; DNA

&lt;213&gt; Conus pulicarius

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(330)

&lt;223&gt; n may be any nucleotide

&lt;400&gt; 213

atgaaactga cgtgtgttgt gatcatcgcc gtgctgttcc tgacggcctg tcaactcatt

60

acagctgaga cttactccag aggttaagcag aagcaccgtg ctttgagggtc aactgacaaa

120

aactccaaatgt gacttaggca gtgctcgct aacgggtggat cttgttctcg tcattttcac

180

tgctgcagcc tctattgcaa taaaaataact ggcgtatgtt ttgcaaccta atacccgtgt

240

gtggcatgaa accactcaat accctctctt ctggaggctt cagaggaact gcattgaaat

300

aaaactgcatttgcacc aaaaaaaaaaaaa

330

&lt;210&gt; 214

&lt;211&gt; 76

&lt;212&gt; PRT

&lt;213&gt; Conus pulicarius

&lt;400&gt; 214

Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
1 5 10 15Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Lys His  
20 25 30

CONUS PULICARIUS

Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys  
 35 40 45

Ser Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys Ser Leu  
 50 55 60

Tyr Cys Asn Lys Asn Thr Gly Val Cys Ile Ala Thr  
 65 70 75

<210> 215  
 <211> 30  
 <212> PRT  
 <213> Conus pulicarius

<220>  
 <221> PEPTIDE  
 <222> (1)..(30)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 is Pro or H  
 yp; Xaa at residue 19 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Ty  
 r, O-sulpho-Tyr or O-phospho-Ty

<400> 215  
 Xaa Cys Ser Xaa Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys  
 1 5 10 15

Ser Leu Xaa Cys Asn Lys Asn Thr Gly Val Cys Ile Ala Thr  
 20 25 30

<210> 216  
 <211> 282  
 <212> DNA  
 <213> Conus purpurascens

<400> 216  
 atgaaaactga cgtgtgtggatcgatcgcc gtgtgttcc tgacggcctg tcaactcatc 60  
 acagctgatg actccagacg tacgcagaag catcgatccc tgaggtcgac caccaaaggc 120  
 gccacgtcga atcgccctg caagacaccc ggacgaaaat gtttccgca tcagaaggac 180  
 tgctcggtc gagcgtgcat catcacaata tgccctgat cttccctt ctgtgctgta 240  
 tcctttctg cctgagtctc cttacctgag agtggtcatg aa 282

<210> 217  
 <211> 72  
 <212> PRT  
 <213> Conus purpurascens

<400> 217  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Gly Ala Thr Ser Asn Arg Pro Cys Lys  
 35 40 45

Thr Pro Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys Cys Gly Arg  
 50 55 60

Ala Cys Ile Ile Thr Ile Cys Pro  
 65 70

<210> 218  
 <211> 27  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 1, 5, 11 and 27 is Pro or Hyp

<400> 218  
 Xaa Cys Lys Thr Xaa Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys  
 1 5 10 15

Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Xaa  
 20 25

<210> 219  
 <211> 340  
 <212> DNA  
 <213> Conus purpurascens

<400> 219  
 accaaaaacca tcatcaaaat gaaactgacg tgggtggtga tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac agctgatgac tccagaggtt cgcagaagca tcgtgccctg 120  
 aggtcgacca ccaaactctt cacgtcgaaa agctgcaagc ttcccgaggc atattgtat 180  
 gcagaagatt atgactgctg ccttagatgc aaagttggag gtacatgtgg ctgatccagt 240  
 gcctgatctt ccccttctg tgctctatcc tttctgcct gagtcctcct tacctaagag 300  
 tggcatgaa ccactcatca ccttctcctc tggaggcttc 340

<210> 220  
 <211> 71  
 <212> PRT  
 <213> Conus purpurascens

<400> 220  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Phe Thr Ser Lys Ser Cys Lys Leu  
 35 40 45

Pro Gly Ala Tyr Cys Asn Ala Glu Asp Tyr Asp Cys Cys Leu Arg Cys  
 50 55 60

Lys Val Gly Gly Thr Cys Gly  
 65 70

<210> 221  
 <211> 26  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> PEPTIDE

<222> (1)..(26)  
 <223> Xaa at residue 12 is Glu or gamma-carboxy Glu; Xaa at residue 5 is Pro or Hyp; Xaa at residue 8 and 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 221  
 Ser Cys Lys Leu Xaa Gly Ala Xaa Cys Asn Ala Xaa Asp Xaa Asp Cys  
 1 5 10 15  
 Cys Leu Arg Cys Lys Val Gly Gly Thr Cys  
 20 25

<210> 222

<211> 317

<212> DNA

<213> Conus purpurascens

<400> 222  
 atgaaaactga cgtgtgtggt gatcgctgcc gtgctgttcc tgacggcctg tcaactcatc 60  
 acagctgatg actccagacg tacgcagaag catcggtgcc tgaggtcgac caccaaacgc 120  
 gcccacgtcga atcgccccctg caagaaaacc ggacgaaaat gttttccgca tcagaaggac 180  
 tgctcggtc gagcgtgcat catcacaata tgccctgtat cttccctt ctgtgctgta 240  
 tcctttctg cctgagtcct ccttacctga gagtggtcat gaaccactca tcaccttctc 300  
 ctctggaggc ttcaagag 317

<210> 223

<211> 72

<212> PRT

<213> Conus purpurascens

<400> 223  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg  
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Arg Ala Thr Ser Asn Arg Pro Cys Lys  
 35 40 45

Lys Thr Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys Cys Gly Arg  
 50 55 60

Ala Cys Ile Ile Thr Ile Cys Pro  
 65 70

<210> 224

<211> 27

<212> PRT

<213> Conus purpurascens

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 1, 11 and 27 is Pro or Hyp

<400> 224

Xaa Cys Lys Lys Thr Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys  
 1 5 10 15

Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Xaa  
 20 25

<210> 225  
 <211> 328  
 <212> DNA  
 <213> Conus radiatus

<400> 225  
 gctgatgcct gatcttcatc gttctccct gtctccttg gcatcaccaa aaccatcatc  
 aaaatgaaac tgacgtgtgt ggtgatcgctc gccgtgctgg tcctgacggc ctgtcaactc  
 atcacagctg atgactccag aggtatgcag aaacatcatg ccctgggtc gatcagcagt  
 ctcttaagt cqaccgcgtca tggctgeaaa cccctcaaac gtcgttgaaa caatgataaa  
 gaatgctgca gcaaattttg caattcagtc cgaaaggcagt gtggataaat ggctaaaaaa  
 ctgaataaaa gcccattgc aaaaaaaaa  
 328

<210> 226  
 <211> 74  
 <212> PRT  
 <213> Conus radiatus

<400> 226  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Val Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Met Gln Lys His His  
 20 25 30

Ala Leu Gly Ser Ile Ser Ser Leu Phe Lys Ser Thr Arg His Gly Cys  
 35 40 45

Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys Cys Ser Lys  
 50 55 60

Phe Cys Asn Ser Val Arg Lys Gln Cys Gly  
 65 70

<210> 227  
 <211> 28  
 <212> PRT  
 <213> Conus radiatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residue 15 is Glu or gamma-carboxy Glu; Xaa at residue 5 is  
 Pro or Hy

<400> 227  
 His Gly Cys Lys Xaa Leu Lys Arg Arg Cys Phe Asn Asp Lys Xaa Cys  
 1 5 10 15

Cys Ser Lys Phe Cys Asn Ser Val Arg Lys Gln Cys  
 20 25

<210> 228  
 <211> 250  
 <212> DNA  
 <213> Conus radiatus

CONUS RADIATUS

<400> 228  
 gaaatgaaac tgacgtgtgt ggtgatcg tcctgacggc ctgtcaactc 60  
 atcacagctg atgactccag aggtatgcag aaacatcatg ccctgggtc gatcagcagt 120  
 ctcttaagt cgaccgtcg tggctgaaa cccctcaaac gtcgttgtt caatgataaa 180  
 gaatgctgca gcaaatttg caattcagtc cgaaaccagt gtggataaat ggctaaaaac 240  
 tgaataaaag 250

<210> 229

<211> 74

<212> PRT

<213> Conus radiatus

<400> 229  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Val Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Met Gln Lys His His  
 20 25 30

Ala Leu Gly Ser Ile Ser Ser Leu Phe Lys Ser Thr Arg Arg Gly Cys  
 35 40 45

Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys Cys Ser Lys  
 50 55 60

Phe Cys Asn Ser Val Arg Asn Gln Cys Gly  
 65 70

<210> 230

<211> 28

<212> PRT

<213> Conus radiatus

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residue 15 is Glu or gamma-carboxy Glu; Xaa at residue 5 is Pro or Hy

<400> 230

Arg Gly Cys Lys Xaa Leu Lys Arg Arg Cys Phe Asn Asp Lys Xaa Cys  
 1 5 10 15

Cys Ser Lys Phe Cys Asn Ser Val Arg Asn Gln Cys  
 20 25

<210> 231

<211> 435

<212> DNA

<213> Conus radiatus

<400> 231

ggaattccgc ttgcacggcg aacctgactt catctttctt ccctgcctcc tttggcatca 60

ccaaaaccat catcaaaatg aaactgacgt gtgtgggtat cgtcggcgtg ctgggtcctga 120

cggcctgtca actcatcaca gctgatgact ccagaggtat gcagaagcat catgccctga 180

ggtcgatcac caaactctcc ctgtcgactc gctgcaaacc tcccggatca ccatgttagag 240

tttcttcgtta taactgctgc tcttcttgca aatcatacaa caagaaatgt ggctgaacctt 300



aaagccacat tgcaaaaaaaaaaaaaaa aa 392  
 <210> 235  
 <211> 74  
 <212> PRT  
 <213> Conus rattus  
 <400> 235  
 Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Cys Gln Phe Asp Thr Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro  
 20 25 30  
 Pro Thr Leu Arg Pro Ala Asp Lys His Ile Arg Leu Thr Lys Arg Cys  
 35 40 45  
 Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser Gly  
 50 55 60  
 Ser Cys Asn Lys Thr Ala Gly Val Cys Leu  
 65 70  
 <210> 236  
 <211> 27  
 <212> PRT  
 <213> Conus rattus  
 <400> 236  
 Cys Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser  
 1 5 10 15  
 Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu  
 20 25  
 <210> 237  
 <211> 395  
 <212> DNA  
 <213> Conus rattus  
 <400> 237  
 ggatccatga aactgacgtg cgtggtgatc atcgccgtgc tgttcctgac agcctgtcaa 60  
 ctcgatgcag ctgcgagcta cgacaaaggt aagcagaaaac ctcctactct gaggccagct 120  
 gacaaaacact tcaggttgat caagcgttgc aatgctcgca atagtggttg cagtcaacat 180  
 cctcaatgct gcagtggatc ttgcaataag actgcaggcg tatgtctgta aagctggct 240  
 gccgtctgat attcccttgc tggctttat cctctttgc ctgagtcatc catacctgtg 300  
 aatggtaag agccactcaa tacctactcc tctggggct tcagaggaac tacattaaat 360  
 aaagccacat tgcaacgaaa aaaaaaaaaa aaaaa 395  
 <210> 238  
 <211> 74  
 <212> PRT  
 <213> Conus rattus  
 <400> 238  
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Asp Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro

20

25

30

Pro Thr Leu Arg Pro Ala Asp Lys His Phe Arg Leu Ile Lys Arg Cys  
 35 40 45

Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser Gly  
 50 55 60

Ser Cys Asn Lys Thr Ala Gly Val Cys Leu  
 65 70

<210> 239

<211> 27

<212> PRT

<213> Conus rattus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 12 is Pro or Hyp

<400> 239

Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Xaa Gln Cys Cys Ser  
 1 5 10 15

Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu  
 20 25

<210> 240

<211> 390

<212> DNA

<213> Conus rattus

<400> 240

ggatccatga aactgacgtg tgtggtgatc atcgccgtgc tggcctgac agcctgtcaa 60

ttcgatacag ctgcgagcta cgacaaaggt aagcagaaac ctcctactct gaggccagct 120

gacaaacact tcaggttgat caagcggtgc aatgctcgca atagtggttg cagtcaacat 180

cctcaatgct gcagtggtat ttgcaataag actttggcg tatgtctgta aagctggct 240

gccgtctgat attcccttgc tggctttat cctctttgc ctgagtcatc catacctgtg 300

aatggtaag agccactcaa tacctactcc tctggggct tcagaggaac tacattaaat 360

aaagccacat tgaa 390

<210> 241

<211> 74

<212> PRT

<213> Conus rattus

<400> 241

Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Phe Asp Thr Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro  
 20 25 30

Pro Thr Leu Arg Pro Ala Asp Lys His Phe Arg Leu Ile Lys Arg Cys  
 35 40 45

Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser Gly  
 50 55 60

Ser Cys Asn Lys Thr Leu Gly Val Cys Leu  
65 70

<210> 242  
<211> 27  
<212> PRT  
<213> Conus rattus

<220>  
<221> PEPTIDE  
<222> (1)..(27)  
<223> Xaa at residue 12 is Pro or Hyp

<400> 242  
Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Xaa Gln Cys Cys Ser  
1 5 10 15

Gly Ser Cys Asn Lys Thr Leu Gly Val Cys Leu  
20 25

<210> 243  
<211> 379  
<212> DNA  
<213> Conus stercusmuscarum

<400> 243  
acccaaaacca tcatcaaaat gaaactgacg tgggtggta tcgtcgccgt gctgctcctg 60  
acggcctgtc aactcatcac agctgatgac tccagaggta cgccagaagca tcgtgcctcg 120  
aggtcgaaga ccaaactctc catgtcgact cgctgcaaga gtaaaggagc aaaatgttca 180  
aggcttatgt atgactgctg cagcggtctc tgccaggct acacaggtag atgtggctga 240  
tccagcgcct gatcttcccc cttctgtgct ctatcctttt ctgcctgggt cctccttacc 300  
tgagagtggt catgaaccac tcacatcaccta ctccctctgga ggcctcagag gagttacaat 360  
gaaataaaag ccgcattgc 379

<210> 244  
<211> 73  
<212> PRT  
<213> Conus stercusmuscarum

<400> 244  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
20 25 30

Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ser  
35 40 45

Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys Ser Gly Ser  
50 55 60

Cys Ser Gly Tyr Thr Gly Arg Cys Gly  
65 70

<210> 245  
<211> 27  
<212> PRT

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<213> Conus stercusmuscarum  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 13 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 245  
 Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Xaa Asp Cys Cys  
 1 5 10 15  
 Ser Gly Ser Cys Ser Gly Xaa Thr Gly Arg Cys  
 20 25

<210> 246

<211> 35  
 <212> PRT  
 <213> Conus stercusmuscarum

<220>  
 <221> PEPTIDE  
 <222> (1)..(35)  
 <223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21, 24 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 246

Thr Thr Ser Cys Met Gln Ala Gly Ser Xaa Cys Gly Ser Thr Thr Arg  
 1 5 10 15  
 Ile Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa  
 20 25 30

Xaa Ser Asn  
 35

<210> 247

<211> 380  
 <212> DNA  
 <213> Conus stercusmuscarum

<400> 247

accaaaaacca tcatcaaaat gaaactgacg tgggtggta tcgtcgccgt gctgctcctg 60  
 acgacacctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg 120  
 aggtcgaaga ccaaactctc catgttaact ttgcgctgac catcttacgg aaaaccttgt 180  
 ggtattgaca acgactgctg caatgcacgc gatccagcca gaaatataatg tacgttagctg 240  
 atccggcgctc tggatcttccc cttctgtgc tctatccttt tctgcctgag tcctccttac 300  
 ctgagagtgg tcatgaacca ctcatcatct actctcctgg aggcctcaga ggagctacaa 360  
 tgaaataaaa gccgcattgc 380

<210> 248

<211> 72  
 <212> PRT  
 <213> Conus stercusmuscarum

<400> 248

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg  
 20 25 30

Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala  
 35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Ala Cys  
 50 55 60

Asp Pro Ala Arg Asn Ile Cys Thr  
 65 70

<210> 249

<211> 26

<212> PRT

<213> Conus stercusmuscarum

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1  
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 249

Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn  
 1 5 10 15

Ala Cys Asp Xaa Ala Arg Asn Ile Cys Thr  
 20 25

<210> 250

<211> 388

<212> DNA

<213> Conus stercusmuscarum

<400> 250

ggatccatga aactgacgtg tgtggtgatt gtcgccgtgc tgctcctgac ggctgtcaa 60  
 ctcatcacag ctgatgactc cagaggtacg caggagcatc gtgcctgag gtcgaagacc  
 aaactctcca tgttaacttt gcgctgcgtc tcttacggaa aaccttggg 120  
 gactgctgca atgcatgcga tccagccaga aatatatgtt cgtagctgat ccggcgtctg  
 atcttcccccc ttctgtgctc tatttttc tgcctgggtc ctccttacct gagagtggtc 180  
 atgaaccact catcacctac tcctctggag gcctcagagg agttacaatg aaataaaagc  
 300  
 cgcattgcaa aaaaaaaaaaaaaaaa 360  
 388

<210> 251

<211> 72

<212> PRT

<213> Conus stercusmuscarum

<400> 251

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg  
 20 25 30

Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Val

35

40

45

Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Ala Cys  
 50 55 60  
 Asp Pro Ala Arg Asn Ile Cys Thr  
 65 70

&lt;210&gt; 252

&lt;211&gt; 26

&lt;212&gt; PRT

&lt;213&gt; Conus stercusmuscarum

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(26)

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<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1  
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

&lt;400&gt; 252

Cys Val Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn  
 1 5 10 15  
 Ala Cys Asp Xaa Ala Arg Asn Ile Cys Thr  
 20 25

&lt;210&gt; 253

&lt;211&gt; 264

&lt;212&gt; DNA

&lt;213&gt; Conus striatus

&lt;400&gt; 253

acccaaaacca tcatcaaaat gaaactgacg tgggtggta tcgtcgccgt gctgctcctg 60  
 acggccctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgttccctg 120  
 aggtcgcacca ccaaagtctc caaggcgact gactgcattg aagccggaaa ttattgcgga 180  
 cctactgtta tgaaaatctg ctgcggctt tgcagtccat acagcaaaat atgtatgaac 240  
 tatccccaaa attgatcttc cccc

&lt;210&gt; 254

&lt;211&gt; 78

&lt;212&gt; PRT

&lt;213&gt; Conus striatus

&lt;400&gt; 254

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg

20

25

30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ala Thr Asp Cys Ile Glu  
 35 40 45

Ala Gly Asn Tyr Cys Gly Pro Thr Val Met Lys Ile Cys Cys Gly Phe  
 50 55 60

Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn Tyr Pro Lys Asn  
 65 70 75

<210> 255  
 <211> 36  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(36)  
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13, 25 and 34 is Pro or Hyp; Xaa at residue 10, 26 and 33 is Tyr, 125 I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 255  
 Ala Thr Asp Cys Ile Xaa Ala Gly Asn Xaa Cys Gly Xaa Thr Val Met  
 1 5 10 15

Lys Ile Cys Cys Gly Phe Cys Ser Xaa Xaa Ser Lys Ile Cys Met Asn  
 20 25 30

Xaa Xaa Lys Asn  
 35

<210> 256  
 <211> 233  
 <212> DNA  
 <213> Conus striatus

<400> 256  
 gtcgactcgc tgcaagctta aaggacaatc atgtcgtagg actatgtatg actgctgcag 60  
 cggttcttgc ggcaggagag gtaaatgtgg ctgatccagc gcctgatctc cccccttctg 120  
 tgctctatcc ttttctgcct gggtcctcct tacctgagag tggtcatgaa ccactcatca 180  
 cctactcctc tggaggcctc agaggagcta caatgaaata aaagccgcat tgc 233

<210> 257  
 <211> 30  
 <212> PRT  
 <213> Conus striatus

<400> 257  
 Ser Thr Arg Cys Lys Leu Lys Gly Gln Ser Cys Arg Arg Thr Met Tyr  
 1 5 10 15

Asp Cys Cys Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys Gly  
 20 25 30

<210> 258  
 <211> 26  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 258  
 Cys Lys Leu Lys Gly Gln Ser Cys Arg Arg Thr Met Xaa Asp Cys Cys  
 1 5 10 15

Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys  
 20 25

<210> 259  
 <211> 310  
 <212> DNA  
 <213> Conus striatus

<400> 259  
 accaaaaacca tcatcaaaat gaaactgacg tgtgtggta tcgtcgccgt gctgctccctg 60  
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgcctcg 120  
 aggtcggaca ccaaactctc catgtcgact cgctgcaagg ctgcaggaaa atcatgcagt 180  
 aggattgcgt ataactgctg caccggttct tgcagatcag gtaaatgcgg ctgatccagc 240  
 gcctgatctt cccccttctg tgctctatcc tttctgcctg agtcccttta-cctgagaytg 300  
 gtcatgaacc 310

<210> 260  
 <211> 71  
 <212> PRT  
 <213> Conus striatus

<400> 260  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30  
 Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ala  
 35 40 45  
 Ala Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser  
 50 55 60  
 Cys Arg Ser Gly Lys Cys Gly  
 65 70

<210> 261  
 <211> 25  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 261  
 Cys Lys Ala Ala Gly Lys Ser Cys Ser Arg Ile Ala Xaa Asn Cys Cys  
 1 5 10 15  
 Thr Gly Ser Cys Arg Ser Gly Lys Cys  
 20 25

<210> 262  
 <211> 256  
 <212> DNA  
 <213> Conus striatus

<400> 262

acccaaaacca tcataaaaaat gaaactgacg tgtgtggta tcgtcgccgt gctgctcctg 60  
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg 120  
 aggtcgacca ccaaactctc catgttaact ttgcgctgcg aatcttacgg aaaaccttg 180  
 ggtatttaca acgactgctg caatgcacgc gatccagcca aaaagacatg tacgttagctg 240  
 atccggcgtc tgatct 256

<210> 263  
 <211> 72  
 <212> PRT  
 <213> Conus striatus

<400> 263  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg  
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Glu  
 35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Ala Cys  
 50 55 60

Asp Pro Ala Lys Lys Thr Cys Thr  
 65 70

<210> 264  
 <211> 26  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residue 2 is Glu or gamma-carboxy Glu; Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 and 11 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 264  
 Cys Xaa Ser Xaa Gly Lys Xaa Cys Gly Ile Xaa Asn Asp Cys Cys Asn  
 1 5 10 15

Ala Cys Asp Xaa Ala Lys Lys Thr Cys Thr  
 20 25

<210> 265  
 <211> 229  
 <212> DNA  
 <213> Conus striatus

<400> 265  
 tcttagtcct ccggcagccc ctgtgggtt actagtatat gctgtggtag atgctataagg 60  
 ggttaaatgtt cgtagctcat cgggcgtctg atcttccccc ttctgtgctc catcctttc 120  
 tgcctgagtc ctccttacct gagagtggtc gtgaaccact catcgctac tcctctggag 180  
 gcttcagagg ggctacacta aaataaaagc tatattgcaa tgaaaaaaa 229

<210> 266  
 <211> 24  
 <212> PRT  
 <213> Conus striatus

<400> 266  
 Cys Arg Ser Ser Gly Ser Pro Cys Gly Val Thr Ser Ile Cys Cys Gly  
 1 5 10 15

Arg Cys Tyr Arg Gly Lys Cys Thr  
 20

<210> 267  
 <211> 24  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(24)  
 <223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 19 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 267  
 Cys Arg Ser Ser Gly Ser Xaa Cys Gly Val Thr Ser Ile Cys Cys Gly  
 1 5 10 15

Arg Cys Xaa Arg Gly Lys Cys Thr  
 20

<210> 268  
 <211> 26  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 268  
 Cys Lys Leu Lys Gly Gln Ser Cys Arg Lys Thr Ser Xaa Asp Cys Cys  
 1 5 10 15

Ser Gly Ser Cys Gly Arg Ser Gly Lys Cys  
 20 25

<210> 269  
 <211> 292  
 <212> DNA  
 <213> Conus striolatus

<400> 269  
 accaaaaacca tcataaaaaat gaaactgacg tgggtggta tcgtcgctt gctgctcctg 60  
 acgacctgtc gtctcatcac agctgatgac tccagaggta cgcagaagca tcgttccctg 120  
 aggtcgacta ctaaagtctc catgtcgact cgctgcaagg gtaaaggagc atcatgtctt 180  
 aggactgcgt atgactgctg caccggttct tgcaacagag gtatgtgg ctgatccagc 240  
 gtctgatctt cccccctctg tgctctatcc ttttctgctt gagtcctcct ta 292

<210> 270  
 <211> 71  
 <212> PRT  
 <213> Conus striolatus

<400> 270  
 Met Lys Leu Thr Cys Val Val Ile Val Val Leu Leu Leu Leu Thr Thr  
 1 5 10 15

Cys Arg Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Met Ser Thr Arg Cys Lys Gly  
 35 40 45

Lys Gly Ala Ser Cys Leu Arg Thr Ala Tyr Asp Cys Cys Thr Gly Ser  
 50 55 60

Cys Asn Arg Gly Arg Cys Gly  
 65 70

<210> 271  
 <211> 25  
 <212> PRT  
 <213> Conus striolatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 271  
 Cys Lys Gly Lys Gly Ala Ser Cys Leu Arg Thr Ala Xaa Asp Cys Cys  
 1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Arg Cys  
 20 25

<210> 272  
 <211> 259  
 <212> DNA  
 <213> Conus striolatus

<400> 272  
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 gcgtgtcaac tcatcacagc tgaggactcc agaggtacac agaagcatcg taccctgagg 120  
 tcgaccgtca gacgctccaa gtccgagttg actacgagat gcaggccttc aggatccaac 180  
 tgtggtaata ttagtatctg ctgtggtaga tgcgttaaca gaagatgtac gtagctcatc 240  
 gggcgtctga tctttcccc 259

<210> 273  
 <211> 71  
 <212> PRT  
 <213> Conus striolatus

<400> 273  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala Cys  
 1 5 10 15

Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Lys His Arg Thr

20

25

30

Leu Arg Ser Thr Val Arg Arg Ser Lys Ser Glu Leu Thr Thr Arg Cys  
 35 40 45

Arg Pro Ser Gly Ser Asn Cys Gly Asn Ile Ser Ile Cys Cys Gly Arg  
 50 55 60

Cys Val Asn Arg Arg Cys Thr  
 65 70

&lt;210&gt; 274

&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Conus striolatus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)...(24)

&lt;223&gt; Xaa at residue 3 is Pro or Hyp

&lt;400&gt; 274

Cys Arg Xaa Ser Gly Ser Asn Cys Gly Asn Ile Ser Ile Cys Cys Gly  
 1 5 10 15

Arg Cys Val Asn Arg Arg Cys Thr  
 20

&lt;210&gt; 275

&lt;211&gt; 280

&lt;212&gt; DNA

&lt;213&gt; Conus striolatus

&lt;400&gt; 275

acccaaaacca tcatcaaaat gaaaactgacg tgggtgggtga tcgtcgccgt tctgttcctg 60

acggcggtgtc aactcatcac agctgaggac tccagaggtt cacagaagca tcgttccctg 120

aggtcgacta ccaaagtctc caagtcgact agctgcattga aagccgggtc ttattgcgtc 180

gctactacga gaatctgctg cggttattgc gcttatttcg gcaaaatatg tattgactat 240

cccaaaaact gatcttcccc ctactgtgct ctatcctttt 280

&lt;210&gt; 276

&lt;211&gt; 77

&lt;212&gt; PRT

&lt;213&gt; Conus striolatus

&lt;400&gt; 276

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys  
 35 40 45

Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg Ile Cys Cys Gly Tyr Cys  
 50 55 60

Ala Tyr Phe Gly Lys Ile Cys Ile Asp Tyr Pro Lys Asn  
 65 70 75

<210> 277

<211> 35  
<212> PRT  
<213> Conus striolatus

<220>

<221> PEPTIDE  
<222> (1)..(35)

<223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21, 24 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 277

Ser Thr Ser Cys Met Lys Ala Gly Ser Xaa Cys Val Ala Thr Thr Arg  
1 5 10 15

Ile Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Ile Cys Ile Asp Xaa  
20 25 30

Xaa Lys Asn  
35

<210> 278  
<211> 174  
<212> DNA  
<213> Conus textile

<400> 278

gttgactcgg tactgcacgc ctcatggagg acattgtggt tatcataatg actgctgcag 60  
tcatcaatgc aatataaaaca gaaataaaatg ttagtagctg atctggcatc tgatctgtgc 120  
tcgtccttac ctgagagtggt tcatgaacca ctcatcacct actcctctgg aggc 174

<210> 279

<211> 31  
<212> PRT  
<213> Conus textile

<400> 279

Leu Thr Arg Tyr Cys Thr Pro His Gly Gly His Cys Gly Tyr His Asn  
1 5 10 15

Asp Cys Cys Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu  
20 25 30

<210> 280

<211> 28  
<212> PRT  
<213> Conus textile

<220>

<221> PEPTIDE  
<222> (1)..(28)

<223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa at residue 4 is Pro or Hyp; Xaa at residue 1 and 11 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 280

Xaa Cys Thr Xaa His Gly Gly His Cys Gly Xaa His Asn Asp Cys Cys  
1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Xaa  
20 25

<210> 281  
 <211> 28  
 <212> PRT  
 <213> Conus textile  
  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa at residue 4 is Pro or Hyp; Xaa at residue 1 and 11 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 281  
 Xaa Cys Thr Xaa Xaa Gly Gly His Cys Gly Xaa His Asn Asp Cys Cys  
 1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Xaa  
 20 25

<210> 282  
 <211> 379  
 <212> DNA  
 <213> Conus tulipa  
  
 <400> 282  
 accaaaaacca tcataaaaaat gaaaactgacg tttgtggta tcgtcgccgt gctgctcctg 60  
 acggcctgtc agctcatcac agctctgcac tccagaggta cgccagaagca tcgtgccctg 120  
 gggcggacca ccaaactcac cttgtcgact cgctgcaaattt caccggatc tccatgttca 180  
 ccgacttagtt ataattgctg ctggtcttgc agtccatata gaaaaaaaaatg taggggctaa 240  
 tccagcgccct gattttcccc cttctgtgct ctattccttt ctgcctgagt cctccttacc 300  
 tgaaagtggc catgaaccac tcatacaccta cttctctgga ggcttcggag gagctacatt 360  
 gaaataaaaag ccgcattgc 379

<210> 283  
 <211> 73  
 <212> PRT  
 <213> Conus tulipa

<400> 283  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Leu His Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Gly Arg Thr Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser  
 35 40 45

Pro Gly Ser Pro Cys Ser Pro Thr Ser Tyr Asn Cys Cys Trp Ser Cys  
 50 55 60

Ser Pro Tyr Arg Lys Lys Cys Arg Gly  
 65 70

<210> 284  
 <211> 27  
 <212> PRT  
 <213> Conus tulipa

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 3, 7, 10 and 21 is Pro or Hyp; Xaa at residue 17 is Trp or Bromo Trp; Xaa at residue 13 and 22 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 284  
 Cys Lys Ser Xaa Gly Ser Xaa Cys Ser Xaa Thr Ser Xaa Asn Cys Cys  
 1 5 10 15  
 Xaa Ser Cys Ser Xaa Xaa Arg Lys Lys Cys Arg  
 20 25

<210> 285

<211> 379

<212> DNA

<213> Conus tulipa

<400> 285

accaaaacca tcatcaaaat gaaactgacg tgggtggta tcgtcgccgt gctgctcctg 60  
 acggcctgtc agctcatcac agctctgcac tccagaggta cgcagaagca tcgtgccctg 120  
 gggtcgacca ccaaactcac cttgtcgact cgctgcttgtt caccggatc ttcatgttca 180  
 ccgactagtt ataattgctg caggtcttgc aatccataca gcagaaaatg taggggctaa 240  
 tccagcgccct gatcttcccc cttctgtgct ctattccctt ctgcctgagt cctccttacc 300  
 tgaaaagtggc catgaaccac tcatcaccta cttctctggc ggcttcggag gagctacatt 360  
 gaaataaaaag ccgcattgc 379

<210> 286

<211> 73

<212> PRT

<213> Conus tulipa

<400> 286

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Leu His Ser Arg Gly Thr Gln Lys His Arg  
 20 25 30

Ala Leu Gly Ser Thr Thr Lys Leu Thr Leu Ser Thr Arg Cys Leu Ser  
 35 40 45

Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys  
 50 55 60

Asn Pro Tyr Ser Arg Lys Cys Arg Gly  
 65 70

<210> 287

<211> 27

<212> PRT

<213> Conus tulipa

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13 and

22 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or  
O-phospho-Ty

<400> 287

Cys Leu Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys  
1 5 10 15  
Arg Ser Cys Asn Xaa Xaa Ser Arg Lys Cys Arg  
20 25

<210> 288

<211> 401

<212> DNA

<213> Conus viola

<400> 288

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acccaaaacca tcataaaaaat gaaactgacg tgggtggta tcgtcgccgt gctgctcctg 60  
acggcctgtc agctcattac agctgatgac tccagaggta cgcagttgca tcgtgccctg 120  
aggaaggcca ccaaactccc cgtgtcact cgctgcatta ctttaggaac acatgtaaag 180  
gttccgagtc aatgctgcag atcttcttgc aagaacggc gttgtgctcc atcccctgaa 240  
gaatggtaaa tggctgat ccagccctg atcttccccc ttctgactgt ctccgaccctt 300  
ttctgcctga gtcctccctta cctgagaggt gtcatgaacc actcatcacc tactccctg 360  
gaagcttcag aggagctaca ttgaaataaaa agccgcattg c 401

<210> 289

<211> 76

<212> PRT

<213> Conus viola

<400> 289

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Leu His Arg  
20 25 30

Ala Leu Arg Lys Ala Thr Lys Leu Pro Val Ser Thr Arg Cys Ile Thr  
35 40 45

Leu Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg Ser Ser Cys  
50 55 60

Lys Asn Gly Arg Cys Ala Pro Ser Pro Glu Glu Trp  
65 70 75

<210> 290

<211> 31

<212> PRT

<213> Conus viola

<220>

<221> PEPTIDE

<222> (1)..(31)

<223> Xaa at residue 29 and 30 is Glu or gamma-carboxy Glu; Xaa at resi  
o Tr due 11, 26 and 28 is Pro or Hyp; Xaa at residue 31 is Trp or Brom

<400> 290

Cys Ile Thr Leu Gly Thr Arg Cys Lys Val Xaa Ser Gln Cys Cys Arg

1	5	10	15
Ser Ser Cys Lys Asn Gly Arg Cys Ala Xaa Ser Xaa Xaa Xaa Xaa			
20 25 30			
<210> 291			
<211> 372			
<212> DNA			
<213> Conus viola			
<400> 291			
acccaaaacca tcatcaaaaat gaaaactgacg tttgtggta tcgtcgccgt gctgctcctg 60			
acggcctgtc agctcattat agctggggac tccagaggtt cgcagttgca tcgtgcctcg 120			
aggaaggcca ccaaactctc cgtgtcqact cgctgcaaga gtagagggatc atcatgtcgt 180			
aggacttcgt atgactgctg cacgggttct tgcagaaatg gtaaatgtgg ctgatccagc 240			
gcctgatctt cccccttctg tgctccatcc ttttctgcct gagtcctcct tacctgagag 300			
tgggcatgaa ccactcatca cctactccct ggaagcttca gaggagctac attgaaataa 360			
aagccgcatt gc			
<210> 292			
<211> 71			
<212> PRT			
<213> Conus viola			
<400> 292			
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala			
1	5	10	15
Cys Gln Leu Ile Ile Ala Gly Asp Ser Arg Gly Thr Gln Leu His Arg			
20 25 30			
Ala Leu Arg Lys Ala Thr Lys Leu Ser Val Ser Thr Arg Cys Lys Ser			
35 40 45			
Arg Gly Ser Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser			
50 55 60			
Cys Arg Asn Gly Lys Cys Gly			
65 70			
<210> 293			
<211> 25			
<212> PRT			
<213> Conus viola			
<220>			
<221> PEPTIDE			
<222> (1)..(25)			
<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty			
<400> 293			
Cys Lys Ser Arg Gly Ser Ser Cys Arg Arg Thr Ser Xaa Asp Cys Cys			
1	5	10	15
Thr Gly Ser Cys Arg Asn Gly Lys Cys			
20 25			

&lt;210&gt; 294

&lt;211&gt; 380

&lt;212&gt; DNA

&lt;213&gt; Conus viola

&lt;400&gt; 294

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acccaaaacca tcatcaaaat gaaactgacg tgggtggcga tcgtcgccgt gctgctcctg 60
acggccgtgc agtcattac agctgaagac tccagaggtt cgcattttttt tcttgcctgt 120
aagtcgacct ccaaagtctc caagtcgact agctgcattttt aagccagatc ttattgcgg 180
cctgctacta cgaaaatctg ctgcgattttt tgcaatccat tcagcgatag atgtatgaac 240
aatcccaaca attgatcttc ccccttgtgt gctccatctt ttctgcctga gtcctcctta 300
cctgagatg gtcatgaacc actcatcacc tactcctctg gagggttcag aggagttaca 360
ttgaaataaa agccgcattgc 380

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&lt;210&gt; 295

&lt;211&gt; 78

&lt;212&gt; PRT

&lt;213&gt; Conus viola

&lt;400&gt; 295

Met	Lys	Leu	Thr	Cys	Val	Ala	Ile	Val	Ala	Val	Leu	Leu	Leu	Thr	Ala
1					5				10					15	

Cys	Gln	Leu	Ile	Thr	Ala	Glu	Asp	Ser	Arg	Gly	Thr	His	Glu	His	Leu
					20			25				30			

Ala	Leu	Lys	Ser	Thr	Ser	Lys	Val	Ser	Lys	Ser	Thr	Ser	Cys	Met	Glu
					35			40			45				

Ala	Arg	Ser	Tyr	Cys	Gly	Pro	Ala	Thr	Thr	Lys	Ile	Cys	Cys	Asp	Phe
	50					55				60					

Cys	Ser	Pro	Phe	Ser	Asp	Arg	Cys	Met	Asn	Asn	Pro	Asn	Asn		
65				70				75							

&lt;210&gt; 296

&lt;211&gt; 36

&lt;212&gt; PRT

&lt;213&gt; Conus viola

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(36)

<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13, 25 and 34 is Pro or Hyp; Xaa at residue 10 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

&lt;400&gt; 296

Ser	Thr	Ser	Cys	Met	Xaa	Ala	Arg	Ser	Xaa	Cys	Gly	Xaa	Ala	Thr	Thr
1					5				10				15		

Lys	Ile	Cys	Cys	Asp	Phe	Cys	Ser	Xaa	Phe	Ser	Asp	Arg	Cys	Met	Asn
					20			25			30				

Asn	Xaa	Asn	Asn		35										
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&lt;210&gt; 297

&lt;211&gt; 373

<212> DNA  
 <213> Conus viola  
  
 <400> 297  
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 aggaagacca ccaaactctc cttgtcgact cgctgcaagg gtccaggagc catatgtata 180  
 aggattgcgt ataactgctg caagtattct tgccggaaatg gttaaatgtgg ctgatccagc 240  
 gcctgatctt ccccttgtg tgctccatcc ttttctgcc tgagtccctcc ttacctgaga 300  
 gtggtcatga accactcatc acctactcct ctggaggctt cagaggagct acattgaaat 360  
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 aaaaagccgca tgc 373

<210> 298  
 <211> 71  
 <212> PRT  
 <213> Conus viola  
  
 <400> 298  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg  
 20 25 30  
 Ala Leu Arg Lys Thr Thr Lys Leu Ser Leu Ser Thr Arg Cys Lys Gly  
 35 40 45  
 Pro Gly Ala Ile Cys Ile Arg Ile Ala Tyr Asn Cys Cys Lys Tyr Ser  
 50 55 60  
 Cys Gly Asn Gly Lys Cys Gly  
 65 70

<210> 299  
 <211> 25  
 <212> PRT  
 <213> Conus viola  
  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 3 is Pro or Hyp; Xaa at residue 13 and 18 is Tyr,  
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T  
 y

<400> 299  
 Cys Lys Gly Xaa Gly Ala Ile Cys Ile Arg Ile Ala Xaa Asn Cys Cys  
 1 5 10 15  
 Lys Xaa Ser Cys Gly Asn Gly Lys Cys  
 20 25

<210> 300  
 <211> 353  
 <212> DNA  
 <213> Conus viola  
  
 <400> 300  
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 aggtcgacca ccaaacactt tatgttgact tggtaactgca cgccatgg aggacattgt 180  
 gtttattata atgactgctg cagtcataa tgcaatataa acagaaataa atgtgagtag 240  
 ctgatccggc atctgatctg tgctgccct aaccctgagag tggtaatgaa ccactcatca 300  
 tctactcctc tggaggcttc agaggagcta catggaaata aaagccgcat tgc 353  
 <210> 301  
 <211> 73  
 <212> PRT  
 <213> Conus viola

<400> 301  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Cys Gln Phe Ile Thr Ala Asp Asp Ser Arg Ser Thr Gln Lys His Arg  
 20 25 30  
 Ala Leu Arg Ser Thr Thr Lys His Phe Met Leu Thr Trp Tyr Cys Thr  
 35 40 45  
 Pro Tyr Gly Gly His Cys Gly Tyr Tyr Asn Asp Cys Cys Ser His Gln  
 50 55 60  
 Cys Asn Ile Asn Arg Asn Lys Cys Glu  
 65 70

<210> 302  
 <211> 28  
 <212> PRT  
 <213> Conus viola

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa at residue 4 is  
 Pro or Hyp; Xaa at residue 1, 5, 11 and 12 is Tyr, 125I-Tyr, mo  
 no-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 302  
 Xaa Cys Thr Xaa Xaa Gly Gly His Cys Gly Xaa Xaa Asn Asp Cys Cys  
 1 5 10 15  
 Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Xaa

<210> 303  
 <211> 294  
 <212> DNA  
 <213> Conus pulicarius

<400> 303  
 ggatccatga aactgacgtg cgtggatt atcgccgtgc tgccctgac ggcctgtcaa 60  
 ctcattacag ctgagactta ctccagagg aagcagatgc accgtgtct gaggtcaact 120  
 gacaaaaact ccaagttgac caggaaatgc acacccctcag atggagcttg tggtttacct 180  
 acacactgct gccccctttt cgtatggca aacaacagat gtctgtaaag cgtctgat 240

tccccttctg tgctctatcc tctttggcct gagtcatcca tacctgtgct cgag 294  
 <210> 304  
 <211> 73  
 <212> PRT  
 <213> Conus pulicarius

<400> 304  
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Met His  
 20 25 30  
 Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Glu Cys  
 35 40 45

---

Thr Pro Pro Asp Gly Ala Cys Gly Leu Pro Thr His Cys Cys Gly Phe  
 50 55 60

Cys Asp Met Ala Asn Asn Arg Cys Leu  
 65 70

<210> 305  
 <211> 27  
 <212> PRT  
 <213> Conus pulicarius

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa at residue 4, 5  
 and 12 is Pro or Hy

<400> 305  
 Xaa Cys Thr Xaa Xaa Asp Gly Ala Cys Gly Leu Xaa Thr His Cys Cys  
 1 5 10 15

Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu  
 20 25

<210> 306  
 <211> 294  
 <212> DNA  
 <213> Conus pulicarius

<400> 306  
 ggatccatga aactgacgtg cgtggtgatt atcgccgtgc tgttcctgac ggcctgtcaa 60  
 ctcattacag ctgagactta ctccagaggt aagcagatgc accgtgctct gaggtcaact  
 gacaaaaact cccagttgac cagggaatgc acacccctccag gtggagcttg tggtttacct 120  
 acacactgct gcggggttttgc cgtatatggca aacaacagat gtctgtaaag cgtctgatat  
 tccccttctg tgctctatcc tctttggcct gagtcatcca tacctgtgct cgag 180  
 <210> 307  
 <211> 73  
 <212> PRT  
 <213> Conus pulicarius

<400> 307  
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Met His  
                   20                         25                         30  
 Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Gln Leu Thr Arg Glu Cys  
                   35                         40                         45  
 Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys Gly Phe  
                   50                         55                         60  
 Cys Asp Met Ala Asn Asn Arg Cys Leu  
                   65                         70

<210> 308  
<211> 27  
<212> PRT

—213— *Conus pulicarius*

<220>  
<221> PEPTIDE  
<222> (1)..(27)  
<223> Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa at residue 4, 5  
and 12 is Pro or Hy

<400> 308

Xaa Cys Thr Xaa Xaa Gly Gly Ala Cys Gly Leu Xaa Thr His Cys Cys  
1 5 10 15

Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu  
20 25

<210> 309

<211> 307

<212> DNA  
<312>  $\hat{m}$

<213> Conus rattus

<400> 309

ggatccatga aactgacgtg tgtggtgatc atcgccgtgc tgttcctggc agcctgtcaa  
cctgttacaa ctgagacttt ctccagaggt aaggagaagc gtcgtgtct gaggtaact  
gacggcaact cccgggttgc cagggcatgc acgcctgaag gtggagcctg tagtagtggg  
cgtcactgct gcggcttttgcgataacgtg tcccacacgt gctatggtga aacaccatct  
ctccactgat gtttccccctt ctgtgtctta tcttcttttgcctgagtcat ccatacctgt  
gctcgaa

<210> 310

<211> 80

<212> PRT

<213> Conus rattus

<400> 310

Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Ala Ala  
1 5 10 15

Cys Gln Pro Val Thr Thr Glu Thr Phe Ser Arg Gly Lys Glu Lys Arg  
20 25 30

Arg Ala Leu Arg Ser Thr Asp Gly Asn Ser Arg Leu Thr Arg Ala Cys  
35 40 45

Thr Pro Glu Gly Gly Ala Cys Ser Ser Gly Arg His Cys Cys Gly Phe

50

55

60

Cys Asp Asn Val Ser His Thr Cys Tyr Gly Glu Thr Pro Ser Leu His  
 65 70 75 80

&lt;210&gt; 311

&lt;211&gt; 34

&lt;212&gt; PRT

&lt;213&gt; Conus rattus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(34)

<223> Xaa at residue 5 and 29 is Glu or gamma-carboxy Glu; Xaa at residue 4 and 31 is Pro or Hyp; Xaa at residue 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

&lt;400&gt; 311

Ala Cys Thr Xaa Xaa Gly Gly Ala Cys Ser Ser Gly Arg His Cys Cys  
 1 5 10 15

Gly Phe Cys Asp Asn Val Ser His Thr Cys Xaa Gly Xaa Thr Xaa Ser  
 20 25 30

Leu His

&lt;210&gt; 312

&lt;211&gt; 342

&lt;212&gt; DNA

&lt;213&gt; Conus stercusmuscarum

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(342)

&lt;223&gt; n may be any nucleotide

&lt;400&gt; 312

agatccatga aactgacgtg cgtggtgatc gtcggcgtgc tgctcctgac ggcctgtcaa 60

ctcatcacag ctgatgactc cagaggtacg caggagcatc gtgcctgag gtcggacacc 120

aaactccccca tatcgactcg ctgcaagggt aaaggagcat catgtcataa gactatgtat 180

gactgctgca gcgggtcctg caccagaggt agatgtggct gatccagcgc ctgatcttcc 240

cccttctgtg ctctatcctt ttctgcctga gtcatcatac ctgtgctcga gcgttactag 300

tggatccgag ctcggtagca agcttggcgt aatcataaaa nc 342

&lt;210&gt; 313

&lt;211&gt; 71

&lt;212&gt; PRT

&lt;213&gt; Conus stercusmuscarum

&lt;400&gt; 313

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg  
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Pro Ile Ser Thr Arg Cys Lys Gly  
 35 40 45

CONUS STERCUSMUSCARUM

Lys Gly Ala Ser Cys His Lys Thr Met Tyr Asp Cys Cys Ser Gly Ser  
 50 55 60

Cys Thr Arg Gly Arg Cys Gly  
 65 70

<210> 314  
 <211> 25  
 <212> PRT  
 <213> Conus stercusmuscarum

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 314  
 Cys Lys Gly Lys Gly Ala Ser Cys His Lys Thr Met Xaa Asp Cys Cys  
 1 5 10 15

Ser Gly Ser Cys Thr Arg Gly Arg Cys  
 20 25

<210> 315  
 <211> 33  
 <212> PRT  
 <213> Conus arenatus

<400> 315  
 Gln Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys  
 1 5 10 15

Ser Leu Tyr Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Tyr  
 20 25 30

Pro

<210> 316  
 <211> 28  
 <212> PRT  
 <213> Conus arenatus

<400> 316  
 Thr Cys Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Arg His Cys Cys  
 1 5 10 15

Ser Gly Tyr Cys His Lys Thr Ile Gln Ala Cys Ser  
 20 25

<210> 317  
 <211> 33  
 <212> PRT  
 <213> Conus arenatus

<400> 317  
 Gln Cys Thr Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys  
 1 5 10 15

Ser Leu Tyr Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Tyr  
 20 25 30

Pro

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<210> 318  
 <211> 33  
 <212> PRT  
 <213> Conus arenatus

<400> 318  
 Gln Cys Thr Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys  
 1 5 10 15  
 Ser Leu Tyr Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Tyr  
 20 25 30  
 Pro

<210> 319  
 <211> 27  
 <212> PRT  
 <213> Conus arenatus

<400> 319  
 Glu Cys Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys  
 1 5 10 15  
 Gly Phe Cys Asp Thr Ala Asn Asn Arg Cys Leu  
 20 25

<210> 320  
 <211> 28  
 <212> PRT  
 <213> Conus arenatus

<400> 320  
 Thr Cys Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Gln His Cys Cys  
 1 5 10 15  
 Ser Gly His Cys His Lys Thr Ile Gln Ala Cys Ala  
 20 25

<210> 321  
 <211> 30  
 <212> PRT  
 <213> Conus arenatus

<400> 321  
 Gln Cys Ser Pro Ile Gly Gly Tyr Cys Thr Leu His Ile His Cys Cys  
 1 5 10 15  
 Ser Asn His Cys Ile Lys Pro Ile Gly Arg Cys Val Ala Thr  
 20 25 30

<210> 322  
 <211> 30  
 <212> PRT  
 <213> Conus arenatus

<400> 322  
 Gln Cys Leu Pro Asn Gly Gly Tyr Cys Thr Leu His Ile His Cys Cys  
 1 5 10 15  
 Ser Asp His Cys Ile Lys Pro Ile Asp Arg Cys Val Ala Thr  
 20 25 30

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<210> 323

<211> 25

<212> PRT

<213> Conus aurisiacus

<400> 323

Cys Lys Gly Lys Gly Lys Pro Cys Ser Arg Ile Ser Tyr Asn Cys Cys  
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
20 25

<210> 324

<211> 32

<212> PRT

<213> Conus aurisiacus

<400> 324

Cys Met Glu Ala Gly Ser Tyr Cys Gly Ser Thr Thr Arg Ile Cys Cys  
1 5 10 15

Gly Phe Cys Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr Pro Ser Asn  
20 25 30

<210> 325

<211> 25

<212> PRT

<213> Conus aurisiacus

<400> 325

Cys Lys Ala Lys Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys  
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
20 25

<210> 326

<211> 26

<212> PRT

<213> Conus aurisiacus

<400> 326

Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn  
1 5 10 15

Ala Cys Asp Pro Gly Arg Asn Ile Cys Thr  
20 25

<210> 327

<211> 36

<212> PRT

<213> Conus bullatus

<400> 327

Ser Thr Ser Cys Met Glu Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr  
1 5 10 15

Lys Ile Cys Cys Asp Phe Cys Ser Pro Phe Ser Asp Arg Cys Met Asn  
20 25 30

Asn Pro Asn Asn  
35

<210> 328

<211> 31

<212> PRT  
 <213> Conus bullatus

<400> 328  
 Cys Ile Thr Pro Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg  
 1 5 10 15  
 Gly Pro Cys Lys Asn Gly Arg Cys Thr Pro Ser Pro Ser Glu Trp  
 20 25 30

<210> 329  
 <211> 26  
 <212> PRT  
 <213> Conus bullatus

<400> 329  
 Cys Ala Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn Asp Cys Cys Asn  
 1 5 10 15  
 Thr Cys Asp Pro Ala Arg Arg Thr Cys Thr

20 25  
 <210> 330  
 <211> 25  
 <212> PRT  
 <213> Conus bullatus

<400> 330  
 Cys Lys Gly Pro Gly Ala Ser Cys Ile Arg Ile Ala Tyr Asn Cys Cys  
 1 5 10 15  
 Lys Tyr Ser Cys Arg Asn Gly Lys Cys

20 25

<210> 331  
 <211> 36  
 <212> PRT  
 <213> Conus bullatus

<400> 331  
 Ser Thr Ser Cys Met Ala Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr  
 1 5 10 15

Asn Ile Cys Cys Asp Phe Cys Ser Pro Phe Ser Asp Arg Cys Met Lys  
 20 25 30

Lys Pro Asn Asn  
 35

<210> 332  
 <211> 25  
 <212> PRT  
 <213> Conus bullatus

<400> 332  
 Cys Lys Ser Lys Gly Ser Ser Cys His Arg Thr Ser Tyr Asp Cys Cys  
 1 5 10 15

Thr Gly Ser Cys Arg Asn Gly Arg Cys  
 20 25

<210> 333  
 <211> 25  
 <212> PRT

TOP SECRET

<213> Conus catus

<400> 333

Cys Lys Ser Thr Gly Ala Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys  
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Arg Cys  
 20 25

<210> 334

<211> 25

<212> PRT

<213> Conus catus

<400> 334

Cys Gln Gly Arg Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys  
 1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Ser Cys  
 20 25

<210> 335

<211> 28

<212> PRT

<213> Conus catus

<400> 335

Cys Leu Pro Ala Gly Glu Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys  
 1 5 10 15

Gly Thr Cys Ser Ser Val Leu Lys Ser Cys Val Ser  
 20 25

<210> 336

<211> 25

<212> PRT

<213> Conus catus

<400> 336

Cys Gln Gly Arg Gly Gly Pro Cys Thr Lys Ala Val Phe Asn Cys Cys  
 1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Arg Cys  
 20 25

<210> 337

<211> 26

<212> PRT

<213> Conus catus

<400> 337

Cys Ala Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn Asp Cys Cys Asn  
 1 5 10 15

Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr  
 20 25

<210> 338

<211> 25

<212> PRT

<213> Conus catus

<400> 338

Cys Arg Gly Arg Gly Gly Pro Cys Thr Lys Ala Met Phe Asn Cys Cys  
 1 5 10 15

TOP SECRET SOURCE

Ser Gly Ser Cys Asn Arg Gly Arg Cys  
20 25

<210> 339  
<211> 33  
<212> PRT  
<213> Conus characteristicus

<400> 339  
Gln Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys  
1 5 10 15

Ser Leu Tyr Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Tyr  
20 25 30

Pro

<210> 340  
<211> 26  
<212> PRT  
<213> Conus consors

<400> 340  
Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn  
1 5 10 15

Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr  
20 25

<210> 341  
<211> 25  
<212> PRT  
<213> Conus consors

<400> 341  
Cys Lys Gly Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys  
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
20 25

<210> 342  
<211> 36  
<212> PRT  
<213> Conus consors

<400> 342  
Ala Thr Asp Cys Ile Glu Ala Gly Asn Tyr Cys Gly Pro Thr Val Met  
1 5 10 15

Lys Ile Cys Cys Gly Phe Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn  
20 25 30

Tyr Pro Gln Asn  
35

<210> 343  
<211> 27  
<212> PRT  
<213> Conus catus

<400> 343  
Cys Lys Gly Lys Gly Ala Ser Cys Thr Arg Leu Met Tyr Asp Cys Cys

100

1

5

10

15

His Gly Ser Cys Ser Ser Ser Lys Gly Arg Cys  
20 25

<210> 344

<211> 25

<212> PRT

<213> Conus consors

<400> 344

Cys Lys Gly Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys  
1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Lys Cys  
20 25

<210> 345

<211> 26

<212> PRT

<213> Conus consors

<400> 345

Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn  
1 5 10 15

Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr  
20 25

<210> 346

<211> 25

<212> PRT

<213> Conus consors

<400> 346

Cys Lys Gly Thr Gly Lys Pro Cys Ser Arg Val Ala Tyr Asn Cys Cys  
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys  
20 25

<210> 347

<211> 35

<212> PRT

<213> Conus consors

<400> 347

Ser Thr Ser Cys Met Lys Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg  
1 5 10 15

Thr Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Phe Cys Ile Asp Phe  
20 25 30

Pro Ser Asn

35

<210> 348

<211> 25

<212> PRT

<213> Conus circumcisus

<400> 348

Cys Lys Gly Lys Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys  
1 5 10 15

Ser Gly Ser Cys Ser Asn Gly Arg Cys  
 20 25

<210> 349

<211> 35

<212> PRT

<213> *Conus circumcisus*

<400> 349

Ser Thr Ser Cys Met Glu Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg  
 1 5 10 15

Thr Cys Cys Gly Tyr Cys Ser Tyr Phe Ser Lys Lys Cys Ile Asp Phe  
 20 25 30

Pro Ser Asn

35

<210> 350

<211> 27

<212> PRT

<213> *Conus circumcisus*

<400> 350

Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys  
 1 5 10 15

Ser Gly Ser Cys Ser Arg Tyr Ser Gly Arg Cys  
 20 25

<210> 351

<211> 35

<212> PRT

<213> *Conus circumcisus*

<400> 351

Ser Thr Gly Cys Met Lys Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg  
 1 5 10 15

Thr Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr  
 20 25 30

Pro Ser Asn

35

<210> 352

<211> 28

<212> PRT

<213> *Conus dalli*

<400> 352

Ser Cys Thr Pro Pro Gly Gly Pro Cys Gly Tyr Tyr Asn Asp Cys Cys  
 1 5 10 15

Ser His Gln Cys Asn Ile Ser Arg Asn Lys Cys Glu  
 20 25

<210> 353

<211> 25

<212> PRT

<213> *Conus distans*

<220>

<221> PEPTIDE

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<222> (1)..(25)  
 <223> Xaa is Hyp

<400> 353  
 Cys Glu Asp Xaa Gly Glu Xaa Cys Gly Ser Asp His Ser Cys Cys Gly  
 1 5 10 15  
 Gly Ser Cys Asn His Asn Val Cys Ala  
 20 25

<210> 354  
 <211> 27  
 <212> PRT  
 <213> Conus ermineus

<400> 354  
 Pro-Cys-Lys-Pro-Lys-Gly-Arg-Lys-Cys-Phe-Pro-His-Gln-Lys-Asp-Cys  
 1 5 10 15  
 Cys Asn Lys Thr Cys Thr Arg Ser Lys Cys Pro  
 20 25

<210> 355  
 <211> 27  
 <212> PRT  
 <213> Conus ermineus

<400> 355  
 Ala Cys Trp Ser Ser Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys  
 1 5 10 15  
 Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn  
 20 25

<210> 356  
 <211> 27  
 <212> PRT  
 <213> Conus geographus

<400> 356  
 Cys Lys Ser Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys  
 1 5 10 15  
 Arg Ser Cys Asn Pro Tyr Ala Lys Arg Cys Tyr  
 20 25

<210> 357  
 <211> 29  
 <212> PRT  
 <213> Conus geographus

<400> 357  
 Cys Lys Ser Pro Gly Thr Pro Cys Ser Arg Gly Met Arg Asp Cys Cys  
 1 5 10 15  
 Thr Pro Cys Leu Leu Tyr Ser Asn Lys Cys Arg Arg Tyr  
 20 25

<210> 358  
 <211> 30  
 <212> PRT  
 <213> Unknown

<220>  
 <223> unknown Conus species

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&lt;400&gt; 358

Cys	Leu	Ser	Pro	Gly	Ser	Arg	Cys	His	Lys	Thr	Met	Arg	Asn	Cys	Cys
1				5					10					15	

Thr	Ser	Cys	Ser	Ser	Tyr	Lys	Gly	Lys	Cys	Arg	Pro	Arg	Lys	
				20				25					30	

&lt;210&gt; 359

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; unknown Conus species

&lt;400&gt; 359

Cys	Lys	Pro	Pro	Gly	Arg	Lys	Cys	Leu	Asn	Arg	Lys	Asn	Glu	Cys	Cys
1				5				10					15		

Ser	Lys	Phe	Cys	Asn	Glu	His	Leu	His	Met	Cys					
			20					25							

&lt;210&gt; 360

&lt;211&gt; 26

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; unknown Conus species

&lt;400&gt; 360

Cys	Lys	Pro	Pro	Arg	Arg	Lys	Cys	Leu	Lys	Ile	Lys	Asp	Lys	Cys	Cys
1				5				10				15			

Asn	Phe	Cys	Asn	Thr	His	Leu	Asn	Met	Cys						
			20				25								

&lt;210&gt; 361

&lt;211&gt; 28

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; unknown Conus species

&lt;400&gt; 361

Cys	Ala	Gly	Pro	Gly	Thr	Ile	Cys	Pro	Asn	Arg	Val	Cys	Cys	Gly	Tyr
1				5				10				15			

Cys	Ser	Lys	Arg	Thr	His	Leu	Cys	His	Ser	Arg	Thr				
			20				25								

&lt;210&gt; 362

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Conus laterculatus

&lt;400&gt; 362

Lys	Cys	Trp	Pro	Ser	Gly	Ser	Tyr	Cys	Arg	Ala	Asn	Ser	Lys	Cys	Cys
1				5				10				15			

Ser	Gly	Cys	Asp	Arg	Asn	Arg	Asn	Lys	Cys	Tyr					
			20				25								

TOEPLITZ

<210> 363  
 <211> 27  
 <212> PRT  
 <213> Conus laterculatus

<400> 363  
 Cys Leu Pro Pro Gly Ser Tyr Cys Lys Ala Thr Thr Glu Val Cys Cys  
 1 5 10 15  
 Ser Ser Cys Leu Gln Phe Ala Gln Ile Cys Ser  
 20 25

<210> 364  
 <211> 30  
 <212> PRT  
 <213> Conus lynceus

<400> 364  
 Cys Lys Ser Pro Gly Ser Pro Cys Ser Val Thr Ser Tyr Asn Cys Cys  
 1 5 10 15  
 Thr Phe Cys Ser Ser Tyr Thr Lys Lys Cys Arg Ala Ser Leu

20 25 30

<210> 365  
 <211> 28  
 <212> PRT  
 <213> Conus lynceus

<400> 365  
 Cys Ala Gly Pro Gly Ala Ile Cys Pro Asn Arg Val Cys Cys Gly Tyr  
 1 5 10 15

Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr  
 20 25

<210> 366  
 <211> 27  
 <212> PRT  
 <213> Conus lynceus

<400> 366  
 Ala Cys Trp Ser Ser Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys  
 1 5 10 15

Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn  
 20 25

<210> 367  
 <211> 27  
 <212> PRT  
 <213> Conus lynceus

<400> 367  
 Lys Cys Trp Ser Pro Gly Thr Tyr Cys Arg Ala His Ser Lys Cys Cys  
 1 5 10 15

Arg Gly Cys Asp Gln Asn Arg Asn Lys Cys Tyr  
 20 25

<210> 368  
 <211> 29  
 <212> PRT  
 <213> Conus laterculatus

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<400> 368  
 Cys Lys Ser Pro Gly Ser Ser Cys Ser Val Ser Met Arg Asn Cys Cys  
 1 5 10 15

Thr Ser Cys Asn Ser Arg Thr Lys Lys Cys Thr Arg Arg  
 20 25

<210> 369

<211> 27

<212> PRT

<213> Conus laterculatus

<400> 369

Thr Cys Trp Pro Ser Gly Thr Ala Cys Gly Ile Asp Ser Asn Cys Cys  
 1 5 10 15

-----  
 Ser Gly Cys Asn Val Ser Arg Ser Lys Cys Asn  
 20 25

<210> 370

<211> 27

<212> PRT

<213> Conus laterculatus

<400> 370

Lys Cys Trp Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys  
 1 5 10 15

Ser Gly Cys Asp Arg Asn Arg Ser Lys Cys Asn  
 20 25

<210> 371

<211> 37

<212> PRT

<213> Conus leopardus

<400> 371

Ser Leu Phe Glu Cys Ala Pro Ser Gly Gly Arg Cys Gly Phe Leu Lys  
 1 5 10 15

Ser Cys Cys Glu Gly Tyr Cys Asp Gly Glu Ser Thr Ser Cys Val Ser  
 20 25 30

Gly Pro Tyr Ser Ile  
 35

<210> 372

<211> 30

<212> PRT

<213> Conus leopardus

<400> 372

Trp Pro Leu Asp Cys Thr Ala Pro Ser Gln Pro Cys Gly Tyr Phe Pro  
 1 5 10 15

Arg Cys Cys Gly His Cys Asp Val Arg Arg Val Cys Thr Ser  
 20 25 30

<210> 373

<211> 31

<212> PRT

<213> Conus leopardus

<400> 373

Cys Met Ser Pro Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Glu

1	5	10	15
Ile Cys Asn Val Tyr Gly Ile Cys Val Ser Asp Leu Pro Gly Ile			
20 25 30			
<210> 374			
<211> 27			
<212> PRT			
<213> Conus leopardus			
<400> 374			
Tyr Cys Ala Pro Pro Gly Gly Ala Cys Gly Phe Phe Asp His Cys Cys			
1	5	10	15
Gly Tyr Cys Glu Thr Phe Tyr Asn Thr Cys Arg			
20 25			

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15	20	25	30
<210> 375			
<211> 25			
<212> PRT			
<213> Conus magus			
<400> 375			
Cys Lys Gly Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys			
1	5	10	15
Thr Gly Ser Cys Arg Ser Gly Lys Cys			
20 25			

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30	35	40	45
<210> 376			
<211> 26			
<212> PRT			
<213> Conus magus			
<400> 376			
Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn			
1	5	10	15
Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr			
20 25			

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50	55	60	65
<210> 377			
<211> 27			
<212> PRT			
<213> Conus miles			
<400> 377			
Cys Asn Asp Arg Gly Gly Cys Ser Gln His Pro His Cys Cys Gly			
1	5	10	15
Gly Thr Cys Asn Lys Leu Ile Gly Val Cys Leu			
20 25			

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70	75	80	85
<210> 378			
<211> 25			
<212> PRT			
<213> Conus monachus			
<400> 378			
Cys Lys Ser Thr Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys			
1	5	10	15
Thr Gly Ser Cys Arg Ser Gly Lys Cys			
20 25			

<210> 379  
 <211> 25  
 <212> PRT  
 <213> Conus monachus

<400> 379  
 Cys Lys Gly Lys Gly Ser Ser Cys Ser Arg Thr Met Tyr Asn Cys Cys  
 1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Lys Cys  
 20 25

<210> 380  
 <211> 35  
 <212> PRT  
 <213> Conus obscurus

<400> 380  
 Ser Pro Pro Cys Met Lys Gly Gly Ser Ser Cys Arg Gly Thr Thr Gly  
 1 5 10 15

Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Tyr Lys Cys Arg Asp Tyr  
 20 25 30

Pro Gln Asn  
 35

<210> 381  
 <211> 28  
 <212> PRT  
 <213> Conus obscurus

<400> 381  
 Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys  
 1 5 10 15

Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser  
 20 25

<210> 382  
 <211> 27  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa is Hyp

<400> 382  
 Xaa Cys Lys Thr Xaa Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys  
 1 5 10 15

Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Pro  
 20 25

<210> 383  
 <211> 26  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residue 5 is Hyp; Xaa at residue 12 is gamma-carboxy-Glu

TOEPLITZ - CONUS

&lt;400&gt; 383

Ser Cys Lys Leu Xaa Gly Ala Tyr Cys Asn Ala Xaa Asp Tyr Asp Cys  
 1 5 10 15

Cys Leu Arg Cys Lys Val Gly Gly Thr Cys  
 20 25

&lt;210&gt; 384

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Conus purpurascens

&lt;400&gt; 384

Pro Cys Lys Lys Thr Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys  
 1 5 10 15

Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Pro  
 20 25

&lt;210&gt; 385

&lt;211&gt; 30

&lt;212&gt; PRT

&lt;213&gt; Conus pulicarius

&lt;400&gt; 385

Gln Cys Ser Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys  
 1 5 10 15

Ser Leu Tyr Cys Asn Lys Asn Thr Gly Val Cys Ile Ala Thr  
 20 25 30

&lt;210&gt; 386

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Conus pulicarius

&lt;400&gt; 386

Glu Cys Thr Pro Pro Asp Gly Ala Cys Gly Leu Pro Thr His Cys Cys  
 1 5 10 15

Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu  
 20 25

&lt;210&gt; 387

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Conus pulicarius

&lt;400&gt; 387

&lt;211&gt; 27

&lt;212&gt; PRT

Glu Cys Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys  
 1 5 10 15

Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu  
 20 25

&lt;210&gt; 388

&lt;211&gt; 28

&lt;212&gt; PRT

&lt;213&gt; Conus radiatus

&lt;400&gt; 388

His Gly Cys Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys  
 1 5 10 15

Cys Ser Lys Phe Cys Asn Ser Val Arg Lys Gln Cys  
 20 25

<210> 389

<211> 28

<212> PRT

<213> Conus radiatus

<400> 389

Arg Gly Cys Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys  
 1 5 10 15

Cys Ser Lys Phe Cys Asn Ser Val Arg Asn Gln Cys  
 20 25

<210> 390

<211> 27

<212> PRT

<213> Conus rattus

<400> 390

Cys Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser  
 1 5 10 15

Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu  
 20 25

<210> 391

<211> 27

<212> PRT

<213> Conus rattus

<400> 391

Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser  
 1 5 10 15

Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu  
 20 25

<210> 392

<211> 27

<212> PRT

<213> Conus rattus

<400> 392

Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser  
 1 5 10 15

Gly Ser Cys Asn Lys Thr Leu Gly Val Cys Leu  
 20 25

<210> 393

<211> 34

<212> PRT

<213> Conus rattus

<400> 393

Ala Cys Thr Pro Glu Gly Gly Ala Cys Ser Ser Gly Arg His Cys Cys  
 1 5 10 15

Gly Phe Cys Asp Asn Val Ser His Thr Cys Tyr Gly Glu Thr Pro Ser  
 20 25 30

Leu His

<210> 394  
 <211> 36  
 <212> PRT  
 <213> Conus striatus

<400> 394  
 Ala Thr Asp Cys Ile Glu Ala Gly Asn Tyr Cys Gly Pro Thr Val Met  
 1 5 10 15  
 Lys Ile Cys Cys Gly Phe Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn  
 20 25 30  
 Tyr Pro Lys Asn  
 35

<210> 395  
 <211> 26  
 <212> PRT  
 <213> Conus striatus

<400> 395  
 Cys Lys Leu Lys Gly Gln Ser Cys Arg Arg Thr Met Tyr Asp Cys Cys  
 1 5 10 15  
 Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys  
 20 25

<210> 396  
 <211> 25  
 <212> PRT  
 <213> Conus striatus

<400> 396  
 Cys Lys Ala Ala Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys  
 1 5 10 15  
 Thr Gly Ser Cys Arg Ser Gly Lys Cys  
 20 25

<210> 397  
 <211> 26  
 <212> PRT  
 <213> Conus striatus

<400> 397  
 Cys Glu Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn  
 1 5 10 15  
 Ala Cys Asp Pro Ala Lys Lys Thr Cys Thr  
 20 25

<210> 398  
 <211> 27  
 <212> PRT  
 <213> Conus stercusmuscarum

<400> 398  
 Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys  
 1 5 10 15  
 Ser Gly Ser Cys Ser Gly Tyr Thr Gly Arg Cys  
 20 25

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<210> 399  
<211> 35  
<212> PRT  
<213> Conus stercusmuscarum

<400> 399  
Thr Thr Ser Cys Met Gln Ala Gly Ser Tyr Cys Gly Ser Thr Thr Arg  
1 5 10 15  
Ile Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr  
20 25 30

Pro Ser Asn  
35

<210> 400  
<211> 26  
<212> PRT  
<213> Conus stercusmuscarum

<400> 400  
Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn  
1 5 10 15  
Ala Cys Asp Pro Ala Arg Asn Ile Cys Thr  
20 25

<210> 401  
<211> 26  
<212> PRT  
<213> Conus stercusmuscarum

<400> 401  
Cys Val Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn  
1 5 10 15  
Ala Cys Asp Pro Ala Arg Asn Ile Cys Thr  
20 25

<210> 402  
<211> 25  
<212> PRT  
<213> Conus stercusmuscarum

<400> 402  
Cys Lys Gly Lys Gly Ala Ser Cys His Lys Thr Met Tyr Asp Cys Cys  
1 5 10 15  
Ser Gly Ser Cys Thr Arg Gly Arg Cys  
20 25

<210> 403  
<211> 25  
<212> PRT  
<213> Conus striolatus

<400> 403  
Cys Lys Gly Lys Gly Ala Ser Cys Leu Arg Thr Ala Tyr Asp Cys Cys  
1 5 10 15  
Thr Gly Ser Cys Asn Arg Gly Arg Cys  
20 25

<210> 404  
<211> 24

<212> PRT  
 <213> Conus striolatus

<400> 404  
 Cys Arg Pro Ser Gly Ser Asn Cys Gly Asn Ile Ser Ile Cys Cys Gly  
 1 5 10 15  
 Arg Cys Val Asn Arg Arg Cys Thr  
 20

<210> 405  
 <211> 35  
 <212> PRT  
 <213> Conus striolatus

<400> 405  
 Ser Thr Ser Cys Met Lys Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg  
 1 5 10 15  
 Ile Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Ile Cys Ile Asp Tyr  
 20 25 30

Pro Lys Asn  
 35

<210> 406  
 <211> 28  
 <212> PRT  
 <213> Conus textile

<400> 406  
 Tyr Cys Thr Pro His Gly Gly His Cys Gly Tyr His Asn Asp Cys Cys  
 1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu  
 20 25

<210> 407  
 <211> 31  
 <212> PRT  
 <213> Conus viola

<400> 407  
 Cys Ile Thr Leu Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg  
 1 5 10 15

Ser Ser Cys Lys Asn Gly Arg Cys Ala Pro Ser Pro Glu Glu Trp  
 20 25 30

<210> 408  
 <211> 25  
 <212> PRT  
 <213> Conus viola

<400> 408  
 Cys Lys Ser Arg Gly Ser Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys  
 1 5 10 15

Thr Gly Ser Cys Arg Asn Gly Lys Cys  
 20 25

<210> 409  
 <211> 36  
 <212> PRT  
 <213> Conus viola

&lt;400&gt; 409

Ser Thr Ser Cys Met Glu Ala Arg Ser Tyr Cys Gly Pro Ala Thr Thr  
 1 5 10 15  
 Lys Ile Cys Cys Asp Phe Cys Ser Pro Phe Ser Asp Arg Cys Met Asn  
 20 25 30  
 Asn Pro Asn Asn  
 35

&lt;210&gt; 410

&lt;211&gt; 25

&lt;212&gt; PRT

&lt;213&gt; Conus viola

&lt;400&gt; 410

Cys Lys Gly Pro Gly Ala Ile Cys Ile Arg Ile Ala Tyr Asn Cys Cys  
 1 5 10 15  
 Lys Tyr Ser Cys Gly Asn Gly Lys Cys  
 20 25

&lt;210&gt; 411

&lt;211&gt; 28

&lt;212&gt; PRT

&lt;213&gt; Conus viola

&lt;400&gt; 411

Tyr Cys Thr Pro Tyr Gly Gly His Cys Gly Tyr Tyr Asn Asp Cys Cys  
 1 5 10 15  
 Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu

20

25

&lt;210&gt; 412

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Conus textile

&lt;400&gt; 412

Cys Thr Pro Tyr Gly Gly His Cys Gly Tyr Asn His Asp Cys Cys Ser  
 1 5 10 15  
 His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu

20

25

&lt;210&gt; 413

&lt;211&gt; 26

&lt;212&gt; PRT

&lt;213&gt; Conus tulipa

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(26)

&lt;223&gt; Xaa is Hyp

&lt;400&gt; 413

Cys Lys Ser Trp Gly Ser Xaa Cys Ser Xaa Thr Ser Thr Asn Cys Cys  
 1 5 10 15  
 Trp Ser Cys Ser Pro Tyr Arg Lys Lys Cys

20

25

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